WEST Search History

DATE: Wednesday, June 19, 2002

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES; OP=OR			
L41	L40 and bicyclic adj nucleotide adj analog?	1	L41
L40	locked adj nucleic adj acid?	39	L40
L39	L38 and lock?	18	L39
L38	L37 and washing	3756	L38
L37	L36 and hybridiz? and RNA	4874	L37
L36	blocking and nucleic adj acid?	9393	L36
L35	blocking	280699	L35
L34	L33 and modified adj nucleotide	21	L34
L33	L32 and (dA or dT)	28	L33
L32	L31 and cDNA	37	L32
L31	L30 and signal?	39	L31
L30	L29 and (probe? or primer?)	50	L30
L29	L28 and base	53	L29
L28	L27 and thymine	53	L28
L27	L26 and adenine	70	L27
L26	L24 and hybridiz?	168	L26
L25	L24 and probe adj nucleotide adj sequence	4	L25
L24	L23 and method?	358	L24
L23	L22 and RNA	367	L23
L22	((dendrimer?) or (branched adj molecule?) or (branched adj polynucleotide?) or (branched adj polynucleic adj acid?))	1290	L22
L21	L20 and lock?	11	L21
L20	modified adj nucleotide	2528	L20
L19	(furanose adj ring) same (nucleic adj acid?)	15	L19
L18	L16 and false adj positive?	2	L18
L17	L16 and lock?	0	L17
L16	L15 and cDNA	11	L16
L15	L14 and L2	23	L15
L14	single adj stranded adj oligonucleotide	1581	L14
L13	L12 and (sodium adj hydroxide)	25	L13
L12	L2 and probe	247	L12

SEARCH REPORT

L11	branch? adj polynucleic adj acid?	0	L11
L10	L2 and microarray?	19	L10
L9	L8 and dendrimer?	1	L9
L8	blocking adj nucleic adj acid?	30	L8
L7	nucleic adj acid adj analogue?	284	L7
L6	L5 same L1	1	L6
L5	locked adj nucleic adj acid?	39	L5
L4	((capture adj nucleotide adj sequence) or (target adj sequence) or (sequence adj of adj interest))	9417	L4
L3	L2 and ((detectable adj signal) or signal)	286	L3
L2	(dendrimer or (branched adj molecule)) and RNA	351	L2
L1	dendrimer?	981	L1

END OF SEARCH HISTORY

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show files
File 155:MEDLINE(R) 1966-2002/Apr W4
File   5:Biosis Previews(R) 1969-2002/Apr W4
         (c) 2002 BIOSIS
File  10:AGRICOLA 70-2002/Apr
         (c) format only 2002 The Dialog Corporation
File  34:SciSearch(R) Cited Ref Sci 1990-2002/May W1
         (c) 2002 Inst for Sci Info
File  35:Dissertation Abs Online 1861-2002/Apr
         (c) 2002 ProQuest Info&Learning
File  50:CAB Abstracts 1972-2002/Apr
         (c) 2002 CAB International
File  65:Inside Conferences 1993-2002/Apr W4
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File  71:ELSEVIER BIOBASE 1994-2002/May W1
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         (c) 2002 Cambridge Sci Abs
File  77:Conference Papers Index 1973-2002/Mar
         (c) 2002 Cambridge Sci Abs
File  94:JICST-EPlus 1985-2002/Mar W2
         (c)2002 Japan Science and Tech Corp(JST)
File 144:Pascal 1973-2002/May W1
         (c) 2002 INIST/CNRS
File 149:TGG Health&Wellness DB(SM) 1976-2002/Apr W3
         (c) 2002 The Gale Group
File 342:Derwent Patents Citation Indx 1978-01/200210
         (c) 2002 Thomson Derwent
File 351:Derwent WPI 1963-2001/UD,UM &UP=200228
         (c) 2002  Thomson Derwent
File 357:Derwent Biotech Res 1982-2002/Feb w3
         (c) 2002 Thomson Derwent & ISI
File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec
         (c) 1998 Inst for Sci Info
File 440:Current Contents Search(R) 1990-2002/May 06
         (c) 2002 Inst for Sci Info
?ds

Set     Items   Description
S1     117574   (NA OR DNA OR NUCLEIC(W)ACID?) (S) (DETERM? OR DETN OR DETG
              OR ASSAY? OR IDENT?)(S)(RIBONUCLEIC(W)ACID? OR RNA)
S2      31744   S1 AND (HYBRID? OR CAPTUR?(4W)REAGENT? OR DENDRIMER?)
S3      27982   S1 (S)(HYBRID? OR CAPTUR?(3W)REAGENT? OR DENDRIMER?)
S4         55   S3 AND LABEL?(5W)SIGNAL?
S5         30   RD (unique items)
?t5/3 ab/1-30
>>>No matching display code(s) found in file(s): 65, 342

 5/AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09940537   99006908   PMID: 9792422
   Fluorescence in situ hybridization using horseradish peroxidase- labeled
 oligodeoxynucleotides and tyramide signal amplification for sensitive
DNA and mRNA detection.
  van de Corput MP; Dirks RW; van Gijlswijk RP; van de Rijke FM; Raap AK
  Department of Molecular Cell Biology, Leiden University Medical Centre.
  Histochemistry and cell biology (GERMANY)  Oct 1998,  110  (4)  p431-7,
ISSN 0948-6143   Journal Code: CDB
```

Languages: ENGLISH
Document type: Journal Article
Record type: Completed

We have used horseradish peroxidase-labeled 40 mer oligodeoxynucleotides (HRP-ODNs) specific for the human cytomegalovirus immediate early gene (HCMV-IE) and a novel dinitrophenol-tyramide signal amplification reagent (DNP-TSA plus) to evaluate their utility in fluorescence in situ hybridization (FISH). For DNA FISH, single or cocktails of HRP-ODNs were hybridized to metaphase chromosomes of rat 9G cells which, as determined by DNA fiber FISH, carry an integrated tandem repeat of 50-60 copies of the HCMV-IE gene. With one layer of DNP-TSA plus deposition and subsequent detection with a fluorochrome-conjugated antibody, four HRP-ODNs were needed to detect the HCMV-IE integration site. When employing two TSA amplification rounds, one HRP-ODN was sufficient for obtaining a strong signal of the integrated gene cluster, indicating that 50-60 HRP molecules can be detected with ease. In addition to DNA FISH, we report here the first use of HRP-ODN probes for mRNA detection by FISH. A single HRP-ODN and one DNP-TSA plus step resulted in clear visualization of the HCMV-IE gene transcripts in rat 9G cells induced for HCMV-IE expression by cycloheximide. Two TSA detection steps enhanced signal intensities even further. Parallel experiments with hapten-labeled ODN and cDNA probes and conventional detection methods illustrated the superiority of the HRP-ODN/TSA approach in DNA and RNA FISH.

5/AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09917787 98449897 PMID: 9774624

Sensitive mRNA detection by fluorescence in situ hybridization using horseradish peroxidase- labeled oligodeoxynucleotides and tyramide signal amplification.

van de Corput MP; Dirks RW; van Gijlswijk RP; van Binnendijk E; Hattinger CM; de Paus RA; Landegent JE; Raap AK

Laboratory for Cytochemistry and Cytometry, Department of Molecular Cell Biology, Leiden University Medical Centre, Leiden, The Netherlands.

journal of histochemistry and cytochemistry (UNITED STATES) Nov 1998, 46 (11) p1249-59, ISSN 0022-1554 Journal Code: IDZ

Languages: ENGLISH
Document type: Journal Article
Record type: Completed

With the ongoing progress in human genome projects, many genes are discovered whose function and/or expression pattern are not known. Most of these genes are expressed in relatively low abundance compared to housekeeping genes such as elongation factor-1alpha and beta-actin. Gene expression is studied by Northern blot assays or by semiquantitative PCR methods. Another method is the visualization of transcripts in tissue or cell cultures by fluorescence in situ hybridization (FISH). However, for low-abundance RNA detection, this method is hampered by its limited detection sensitivity and by the interference of background signals with specific hybridization signals. Background signals are introduced by nonspecific hybridization of probe sequences or nonspecific binding of antibodies used for visualization. To eliminate background signals derived from both sources and to benefit from the peroxidase-driven tyramide signal amplification (TSA), we directly conjugated horseradish peroxidase (HRP) to oligodeoxynucleotides (ODNs) and used these probes to study in the bladder cancer cell line 5637 the expression of various cytokine genes which, according to Northern hybridization and reverse transcriptase-polymerase chain reaction (RT-PCR) assays , are expressed at levels up to 10,000-fold less than abundantly expressed housekeeping genes. The results show that reduction of probe complexity and the limited use of immunocytochemical

detection layers strongly reduces noise signals derived from nonspecific binding of nucleic acid probe and antibodies. The use of the HRP-ODNs in combination with TSA allowed detection of low-abundance cytokine mRNAs by FISH.

5/AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09902880 98397534 PMID: 9728288
High performance Nanogold-silver in situ hybridisation.
Hacker GW
Institute of Pathological Anatomy, Salzburg General State Hospital, University of Salzburg, Austria. g.hacher@lkasbg.gv.at
European journal of histochemistry (ITALY) 1998, 42 (2) p111-20, ISSN 1121-760X Journal Code: BAL
Languages: ENGLISH
Document type: Journal Article; Review; Review, Tutorial
Record type: Completed
Conventional in situ hybridisation (ISH) usually requires the presence of at least 10-50 copies of the nucleic acid sequence in question per cell. In situ PCR has been proposed as an alternative method, which may yield single-copy sensitivity, but shows a relatively high rate of false-negative or even false-positive reactions. Very recently, possible alternatives have been described, which can be performed in routine laboratories without the need for expensive equipment. Streptavidin-Nanogold-Silver ISH is an easy-to-perform assay , which can be applied to detect low copy numbers of nucleic acid sequences in paraffin sections and cytological preparations. Its combination with labelled tyramides (TSATM = tyramide signal amplification, also known as CARD = catalysed reporter deposition) can achieve single gene copy sensitivity in detecting DNA viruses and also shows very high sensitivity for RNA detection. Possible applications include the early recognition of viral infection, cancer-associated genes, genetic diseases, and also the specific detection of mRNA.

5/AB/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08012558 94092466 PMID: 7903544
Quantitative and sensitive northern blot hybridization using PCR-generated DNA probes labeled with digoxigenin by nick translation.
Sato M; Murao K; Mizobuchi M; Takahara J
First Department of Internal Medicine, Kagawa Medical School, Miki-Cho, Japan.
BioTechniques (UNITED STATES) Nov 1993, 15 (5) p880-2, ISSN 0736-6205 Journal Code: AN3
Languages: ENGLISH
Document type: Technical Report
Record type: Completed
Northern blot hybridization is one of the most convenient methods of detecting an mRNA. Nonradioactive Northern blotting using digoxigenin (DIG) is becoming widely applied because it is rapid and safe. Previous studies have indicated that DIG-labeled RNA probes are suitable for Northern blot hybridization . Here, the application of PCR-generated double-stranded DNA probes labeled with DIG by nick translation is described. DNA probes were synthesized by PCR, then labeled with DIG by nick translation. Northern blot hybridization was performed using the DIG- labeled DNA probes, and the signals were detected by means of a chemiluminescent reaction. A low amount of DIG-dUTP in the labeling reaction resulted in

excellent Northern blots with low background. Densitometric analysis of the blots showed that the mRNA concentrations could be determined by densitometric analysis. The sensitivity of the DIG-Northern system was comparable to Northern blotting using 32P and was sufficiently sensitive to detect low-abundance mRNA.

5/AB/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07025177 93126302 PMID: 8419910
Cortivazol increases glucocorticoid receptor expression and inhibits growth of hamster pancreatic cancer (H2T) in vivo.
Evers BM; Thompson EB; Townsend CM; Lawrence JL; Johnson B; Srinivasan G; Thompson JC
Department of Surgery, University of Texas Medical Branch, Galveston 77550.
Pancreas (UNITED STATES) Jan 1993, 8 (1) p7-14, ISSN 0885-3177 Journal Code: PRS
Contract/Grant No.: 5R37 DK 15241, DK, NIDDK; CA 41407, CA, NCI; PO1 DK 35608, DK, NIDDK
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Glucocorticoids are effective in the treatment of certain leukemias and lymphomas, but their effects on the growth of several solid tumors have not been determined . We report here that cortivazol (CVZ), a potent synthetic glucocorticoid, inhibits the growth of a hamster pancreatic adenocarcinoma, H2T, in vivo. CVZ regulation of glucocorticoid receptor (GR) expression was followed as a specific molecular correlate. H2T cells were injected into cheek pouches of male Syrian golden hamsters, where they formed readily measurable tumors. Two studies were performed. In the first, hamsters were randomized to three groups immediately after injection of tumor cells: control, CVZ (0.1 micrograms/g body wt), or CVZ (0.3 micrograms/g body wt). Injections of either CVZ or its vehicle were administered on a 14-day cycle of 5 treatment days, followed by 9 days off treatment. Tumors were measured and areas calculated weekly. On day 48, the hamsters were killed and the tumors excised, weighed, and analyzed for DNA , RNA , and protein content. In the second study, randomization and treatment schedule were as before, except that on day 33 the hamsters were killed, tumors were excised and weighed, and total RNA from the tumors was isolated. GR mRNA content was determined by filter hybridization with a 32P- labeled GR cDNA probe, and the signal normalized by reprobing for alpha-tubulin as an invariant, independent signal. At either dose, CVZ significantly inhibited H2T tumor area and weight and DNA , RNA , and protein content. Body weights of animals treated with CVZ were not significantly decreased as compared with controls. In addition, GR mRNA in H2T cells was increased approximately twofold by CVZ.(ABSTRACT TRUNCATED AT 250 WORDS)

5/AB/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05367571 90129910 PMID: 2613556
Non-isotopic RNA probes. Comparison between different labels and detection systems.
Giaid A; Hamid Q; Adams C; Springall DR; Terenghi G; Polak JM
Department of Histochemistry, Royal Postgraduate Medical School, Hammersmith Hospital, London, UK.
Histochemistry (GERMANY, WEST) 1989, 93 (2) p191-6, ISSN 0301-5564 Journal Code: G9K

Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Several studies have shown the use of non-radioactive labelled DNA probes for in situ hybridisation , mainly to identify cellular DNA . In this study mRNA in situ hybridisation was performed on rat pituitary with biotinylated complementary (c) RNA probes for rat prolactin and growth hormone (GH), and compared with radioactive 35S-radiolabelled probes. Biotinylated cRNA probes were labelled with either biotin-11-UTP or with allylamine-UTP, the latter method being able to produce a higher yield of labelled RNA . Different detection systems were tested, and hybridisation signal was seen in cells of anterior pituitary with both types of biotinylated probes. The signals were detected using either avidin-biotin-complex with peroxidase (ABC), peroxidase-anti-peroxidase (PAP) or gold-silver methods. ABC peroxidase detected using glucose oxidase-diaminobenzidine (DAB)-nickel solution appeared to be the best method for detecting labelled RNA probes, with very strong signal and low background. The biotinylated probes were comparable in sensitivity to the radiolabelled probes in detecting prolactin and GH mRNAs in the anterior lobe of the rat pituitary. These results indicate an alternative methods of labelling and detection of biotinylated probes which could have a potential role in research and diagnostic techniques.

5/AB/7 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11697802 BIOSIS NO.: 199800479533
High performance nanogoldTM-silver in situ hybridisation.
AUTHOR: Hacker G W(a)
AUTHOR ADDRESS: (a)Inst. Pathological Anat., Immunohistochem. Biochem. Unit, Salzburg Gen. State Hosp., Univ. Salzb**Austria
JOURNAL: European Journal of Histochemistry 42 (2):p111-120 1998
ISSN: 1121-760X
DOCUMENT TYPE: Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Conventional in situ hybridisation (ISH) usually requires the presence of at least 10-50 copies of the nucleic acid sequence in question per cell. In situ PCR has been proposed as an alternative method, which may yield single-copy sensitivity, but shows a relatively high rate of false-negative or even false-positive reactions. Very recently, possible alternatives have been described, which can be performed in routine laboratories without the need for expensive equipment. Streptavidin-Nanogold-Silver ISH is an easy-to-perform assay , which can be applied to detect low copy numbers of nucleic acid sequences in paraffin sections and cytological preparations. Its combination with labelled tyramides (TSATM = tyramide signal amplification, also known as CARD = catalysed reporter deposition) can achieve single gene copy sensitivity in detecting DNA viruses and also shows very high sensitivity for RNA detection. Possible applications include the early recognition of viral infection, cancer-associated genes, genetic diseases, and also the specific detection of mRNA.

1998

5/AB/8 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11691141 BIOSIS NO.: 199800472872
Fluorescence in situ hybridization using horseradish peroxidase- labeled oligodeoxynucleotides and tyramide signal amplification for sensitive DNA and mRMA detection.
AUTHOR: van De Corput Mariette P C; Dirks Roeland W; Van Gijlswijk Rob P M; Van De Rijke Frans M; Raap Anton K(a)
AUTHOR ADDRESS: (a)Lab. Cytochem. Cytometry, Dep. Mol. Cell Biol., Leiden Univ. Med. Centre, Wassenaarseweg 72, NL-**Netherlands
JOURNAL: Histochemistry and Cell Biology 110 (4):p431-437 Oct., 1998
ISSN: 0948-6143
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We have used horseradish peroxidase-labeled 40 mer oligodeoxynucleotides (HRP-ODNs) specific for the human cytomegalovirus immediate early gene (HCMV-IE) and a novel dinitrophenol-tyramide signal amplification reagent (DNP-TSA plus) to evaluate their utility in fluorescence in situ hybridization (FISH). For DNA FISH, single or cocktails of HRP-ODNs were hybridized to metaphase chromosomes of rat 9G cells which, as determined by DNA fiber FISH, carry an integrated tandem repeat of 50-60 copies of the HCMV-IE gene. With one layer of DNP-TSA plus deposition and subsequent detection with a fluorochrome-conjugated antibody, four HRP-ODNs were needed to detect the HCMV-IE integration site. When employing two TSA amplification rounds, one HRP-ODN was sufficient for obtaining a strong signal of the integrated gene cluster, indicating that 50-60 HRP molecules can be detected with ease. In addition to DNA FISH, we report here the first use of HRP-ODN probes for mRNA detection by FISH. A single HRP-ODN and one DNP-TSA plus step resulted in clear visualization of the HCMV-IE gene transcripts in rat 9G cells induced for HCMV-IE expression by cycloheximide. Two TSA detection steps enhanced signal intensities even further. Parallel experiments with hapten-labeled ODN and cDNA probes and conventional detection methods illustrated the superiority of the HRP-ODN/TSA approach in DNA and RNA FISH.

1998

5/AB/9 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11537018 BIOSIS NO.: 199800318350
Molecular biological methods to detect "Microthrix parvicella" and to determine its abundance in activated sludge.
AUTHOR: Bradford Debbie(a); Christensson Camilla; Jakab Nicole(a); Blackall Linda L(a)
AUTHOR ADDRESS: (a)Adv. Wastewater Management Centre, Dep. Microbiol., Univ. Queensl., Brisbane**Australia
JOURNAL: Water Science and Technology 37 (4-5):p37-45 Feb.-March, 1998
ISSN: 0273-1223
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Molecular biological methods were evaluated in attempts to detect and quantitate levels of "Microthrix parvicella" in activated sludges. Approximately 66% of the 23S rRNA gene sequence of a strain (Ben43) of

the Gram positive bulking and foaming organism "Microthrix parvicella" was determined , while a lesser amount was determined for "M. parvicella" strain RN1. The high mol%G+C Gram positive bacteria (HGCGPBs) possess two powerfully diagnostic regions in the 23S rDNA and these were investigated in both strains. Firstly, the 18 nucleotide HGCGPB probe sequence (HGC69a) varied in at least two nucleotides with the sequence from both strains of "M. parvicella". Secondly, an approximately 100 nucleotide stable insert between helices 54 and 55 in the 23S rRNA of HGCGPBs was discovered to be present in "M. parvicella", but in both strains it was unique in length (79 nucleotides) and sequence. The region of the 23S rDNA with the stable insert was exploited to develop a polymerase chain reaction assay in which amplicons from "M. parvicella" were larger than those from nonHGCGPBs (i.e. all Bacteria except the HGCGPBs), and smaller than those from HGCGPBs. This assay was evaluated with DNAs extracted from activated sludges but although "M. parvicella" was morphologically identified , and was a dominant filament in at least one of the samples, no "M. parvicella" specific sized amplicons could be recovered from it. Amplicons of sizes generated by nonHGCGPBs and HGCGPBs were routinely produced in the stable insert PCR with DNAs from activated sludges where the highest yield was of amplicons from nonHGCGPBs. A second series of experiments were undertaken with the objective of evaluating the use of a non-radioactive hybridization method, based on extraction of bacterial RNA , for quantifying "M. parvicella" in activated sludge samples. Total nucleic acids were extracted from activated sludge samples and immobilized on nylon membranes. Probing with 16S rRNA-directed DIG- labelled oligonucleotide probes, detection of chemiluminescent signals on membranes and densitometry allowed hybridization signals to be quantified. The relationship between the amount of nucleic acid hybridized and the hybridization signal intensity observed was found to be linear over a specified range of signal intensities. A range of activated sludge samples were analysed for "M. parvicella" and variations in levels could be distinguished.

1998

5/AB/10 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

05637999 Genuine Article#: WM672 Number of References: 21
Title: Sensitive nonradioactive dot blot/ribonuclease protection assay for quantitative determination of mRNA (ABSTRACT AVAILABLE)
Author(s): Zhan JH; Fahimi HD; Voelkl A (REPRINT)
Corporate Source: UNIV HEIDELBERG,DEPT ANAT & CELL BIOL 2, INF 307/D-69120 HEIDELBERG//GERMANY/ (REPRINT); UNIV HEIDELBERG,DEPT ANAT & CELL BIOL 2/D-69120 HEIDELBERG//GERMANY/
Journal: BIOTECHNIQUES, 1997, V22, N3 (MAR), P500-&
ISSN: 0736-6205 Publication date: 19970300
Publisher: EATON PUBLISHING CO, 154 E. CENTRAL ST, NATICK, MA 01760
Language: English Document Type: ARTICLE
Abstract: We have developed a simple and sensitive method for the rapid quantitation of mRNA from a cell cultures and small tissue samples. The method combines the high sensitivity and specificity of the ribonuclease protection assay with simple handling and rapid execution of dot blotting. The use of digoxygenin-labeled cRNA probes eliminates all problems associated with radioisotopes commonly used in the ribonuclease protection assay. The RNA preparation is dotted directly onto nylon membranes, and after hybridization the filters are treated with ribonuclease A, which remove the nonhybridized single-stranded RNA. The mRNA-hybrid is then visualized by the chemiluminescence

technique using labeled anti-diogoxigenin antibody, and the signal intensity is quantitated. Comparison with the Northern blotting ribonuclease protection assay revealed that this dot blot technique is almost ten times more sensitive and that its signals are linear over a wide range of RNA concentrations (0.01-10 mu g/mu L/dot). This method seems particularly valuable for simultaneous processing of large numbers of samples containing a wide range of RNA concentrations.

5/AB/11 (Item 1 from file: 149)
DIALOG(R)File 149:TGG Health&Wellness DB(SM)

01413886 SUPPLIER NUMBER: 13566265 (USE FORMAT 7 OR 9 FOR FULL TEXT)
Higher level organization of individual gene transcription and RNA splicing.
Yigong Xing; Johnson, Carol V.; Dobner, Paul R.; Lawrence, Jeanne Bentley
Science, v259, n5099, p1326(5)
Feb 26,
1993
PUBLICATION FORMAT: Magazine/Journal ISSN: 0036-8075 LANGUAGE: English
RECORD TYPE: Fulltext; Abstract TARGET AUDIENCE: Academic
WORD COUNT: 3673 LINE COUNT: 00293

AUTHOR ABSTRACT: Visualization of fibronectin and neurotensin messenger RNAs within mammalian interphase nuclei was achieved by fluorescence hybridization with genomic, complementary DNA, and intron-specific probes. Unspliced transcripts accumulated in one or two sites per nucleus. Fibronectin RNA frequently accumulated in elongated tracks that overlapped and extended well beyond the site of transcription. Splicing appears to occur directly within this RNA track, as evidenced by an unambiguous spatial separation of intron-containing and spliced transcripts. Excised introns for neurotensin RNA appear free to diffuse. The transcription and processing site of the fibronectin gene localized to the nuclear interior and was associated with larger transcript domains in over 88 percent of the cells. These results support a view of nuclear function closely integrated with structure.

5/AB/12 (Item 2 from file: 149)
DIALOG(R)File 149:TGG Health&Wellness DB(SM)

01235093 SUPPLIER NUMBER: 08305415 (USE FORMAT 7 OR 9 FOR FULL TEXT)
High-resolution mapping of human chromosome 11 by in situ hybridization with cosmid clones.
Lichter, Peter; Chang Tang, Chieh-Ju; Call, Katherine; Hermanson, Gary; Evans, Glen A.; Housman, David; Ward, David C.
Science, v247, n4938, p64(6)
Jan 5,
1990
PUBLICATION FORMAT: Magazine/Journal ISSN: 0036-8075 LANGUAGE: English
RECORD TYPE: Fulltext; Abstract TARGET AUDIENCE: Academic
WORD COUNT: 4837 LINE COUNT: 00454

ABSTRACT: The gene is the basic unit of heredity and occurs in pairs called alleles on chromosomes, thread-like structures in the nucleus. There are 23 pairs of chromosomes in each cell. The genetic information is carried by deoxyribonucleic acid (DNA) and processed into proteins by the ribonucleic acids (RNA). DNA consists of nucleotide subunits, made up of a deoxyribose sugar, phosphate, and one of the four bases: adenine,

guanine, cytosine and thymine. The nucleotides link together by their phosphate groups to make up a strand. Two strands of nucleotides bind together by complementary base pairs; in other words, certain bases always bind to each other. For example, the guanine base from one strand always binds to the cytosine base of the other strand, and adenine always binds to thymine. This characteristic of complementary base pairing can be used to determine an unknown nucleotide sequence in a single strand of DNA . The strand containing the unknown sequence of nucleotide is isolated and exposed to strands of DNA containing known sequences of nucleotides; the known sequence that is bound will reflect the unknown sequence of nucleotides. Current research is intensively focused on mapping the human chromosomes, and this knowledge may be used to understand and treat genetic diseases, including some forms of cancer. This study uses a modified form of the hybridization method to map the human chromosome 11.

5/AB/13 (Item 1 from file: 351)
DIALOG(R)File 351:Derwent WPI

014366981
WPI Acc No: 2002-187683/200224
Related WPI Acc No: 1998-610000
XRAM Acc No: C02-057862
Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognasticating, preventing or treating or determining predisposition to prostate disease
Patent Assignee: BILLINGEL P A (BILL-I); COHEN M (COHE-I); COPLPITTS T L (COPL-I); FRIEDMAN P N (FRIE-I); GORDON J (GORD-I); GRANADOS E N (GRAN-I); HODGES S C (HODG-I); KLASS M R (KLAS-I); KRATOCHVIL J D (KRAT-I); ROBERTS-RAPP L (ROBE-I); RUSSELL J C (RUSS-I); STROUPE S D (STRO-I)
Inventor: BILLINGEL P A; COHEN M; COPLPITTS T L; FRIEDMAN P N; GORDON J; GRANADOS E N; HODGES S C; KLASS M R; KRATOCHVIL J D; ROBERTS-RAPP L; RUSSELL J C; STROUPE S D
Number of Countries: 001 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
US 20010055758	A1	20011227	US 97842385	A	19970423	200224 B
			US 9865383	A	19980423	

Priority Applications (No Type Date): US 9865383 A 19980423; US 97842385 A 19970423
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
US 20010055758	A1		57	C12Q-001/68	CIP of application US 97842385

Abstract (Basic): US 20010055758 A1
Abstract (Basic):

NOVELTY - Detecting the presence of a target PS118 polynucleotide in a test sample, is new.

DETAILED DESCRIPTION - Detecting (M1) the presence of a target PS118 polynucleotide in a test sample comprising:

(a) contacting the sample with at least one PS118-specific polynucleotide (PN) or its complement; and

(b) detecting the presence of the target PS118 PN, which has at least 50% identity with a fully defined sequence selected from sequences (I-X) as given in the specification and their fragments or complements, is new.

INDEPENDENT CLAIMS are also included for the following:

(1) detecting (M2) mRNA of PS118 in a test sample comprising:

(a) performing reverse transcriptase (RT) with at least one primer

in order to produce cDNA;

(b) amplifying the cDNA obtained from step (a) using PS118 oligonucleotides (OGN) as (anti)sense primers to obtain PS118 amplicon; and

(c) detecting the presence of PS118 amplicon in the test sample where the PS118 OGNs utilized in steps (a) and (b) have at least 50% identity with a sequence selected from (I-X) and fragments or complements of this;

(2) detecting (M3) a target PS118 PN in a test sample comprising

(a) contacting the test sample with at least one PS118 OGN as a sense primer and with at least one PS118 OGN as an anti-sense primer and amplifying to obtain a first stage reaction product;

(b) contacting the first stage reaction product with at least one other PS118 OGN to obtain a second stage reaction product with the proviso that the other PS118 OGN is located 3' to the PS118 OGNs utilized in step (a) and is complementary to the first stage reaction product; and

(c) detecting the second stage reaction product as an indication of the presence of the target PS118 PN where the PS118 OGNs utilized in steps (a) and (b) have at least 50% identity with a sequence selected from (I-X) and fragments or complements of this;

(3) a test kit (K1) for detecting PS118 PN in a test sample, comprising a container containing at least one PS118 PN having at least 50% identity with a sequence selected from the group of sequences (I-X)/fragments/complements;

(4) a purified PN or fragment derived from a PS118 gene where the PN is capable of selectively hybridizing to the nucleic acid of the PS118 gene and has at least 50% identity with a PN selected from the group consisting of sequences (I-IV), sequences (VII -X) and complements and fragments of (I-VIII);

(5) a recombinant expression system comprising a nucleic acid sequence that includes an open reading frame derived from PS118 operably linked to a control sequence compatible with a desired host where the nucleic acid sequence has at least 50% identity with sequences (I-X)/fragments/complements;

(6) a cell transfected with the recombinant expression system of claim (5);

(7) a PS118 polypeptide having at least 50% identity with an amino acid sequence selected from the group consisting of sequences (XI), (XII), (XIII), (XIV), (XV) and fragments of these;

(8) an antibody (Ab) which specifically binds to at least one PS118 epitope which is derived from an amino acid sequence having at least 50% identity with sequences (XI-XV) or fragments of these;

(9) assay kit (K2) for determining the presence of PS118 antigen (Ag) or anti-PS118 Ab in a test sample, comprising a container containing an Ab which specifically binds to a PS118 Ag that comprises at least one PS118 epitope;

(10) producing (M4) a polypeptide comprising at least one PS118 epitope, by incubating host cells that have been transfected with an expression vector containing a PN sequence encoding a polypeptide, where the polypeptide comprises an amino acid sequence having at least 50% identity with the group of sequences (XI-XV) and fragments of these;

(11) detecting (M5) PS118 Ag in a test sample suspected of containing the PS118 Ag comprising:

(a) contacting the test sample with an antibody or fragment which specifically binds to at least one epitope of a PS118 Ag selected from the group of sequences (XI-XV) and fragments of these where the contacting is carried out for a time and under conditions sufficient for the formation of antibody/antigen complexes; and

(b) detecting the complexes;

(12) detecting (M6) the presence of Abs specific for a PS118 Ag in a test sample comprising:

(a) contacting the test sample with PS118 polypeptide which contains at least one epitope derived from an amino acid sequence or fragment having at least 50% identity with a sequence selected from the group of sequences (XI-XV) and fragments of these where the contacting is carried out for a time and under conditions sufficient for the formation of antibody/antigen complexes; and

(b) detecting the complexes;

(13) cell transfected with a nucleic acid sequence encoding at least one PS118 epitope where the nucleic acid is selected from the group of sequences (I-X)/fragments/complements;

(14) producing (M7) Abs which specifically bind to PS118 Ag comprising:

(a) administering to an individual an isolated immunogenic polypeptide or fragment in an amount sufficient to elicit an immune response, where the immunogenic polypeptide comprises at least one PS118 epitope and has at least 50% identity with a sequence from the group of sequences (XI-XV) and fragments of these; or

(b) administering to an individual a plasmid comprising a sequence which encodes at least one PS118 epitope derived from a polypeptide having an amino acid sequences selected from the group of sequences (XI-XV) and fragments of these;

(15) a composition of matter comprising:

(a) a PS118 PN or fragment where the PN has at least 50% identity with a PN selected from the group consisting of sequences (I-IV), sequences (VII -X) and complements and fragments of (I-VIII); or

(b) a polypeptide containing at least one PS118 epitope and has at least 50% identity with a sequence from the group of sequences (XI-XV) and fragments of these;

(16) a gene (fragment) which codes for a PS118 protein which comprises an amino acid sequence having at least 50% identity to sequence (XI); and

(17) a gene (fragment) comprising DNA having at least 50% identity with sequence (IX) or (X).

ACTIVITY - Cytostatic. No biodata is given.

MECHANISM OF ACTION - None given in the source material.

USE - The invention provides methods and reagents which are useful for detecting, diagnosing, staging, monitoring, prognasticating, preventing or treating or determining the predisposition of an individual to diseases and conditions of the prostate. Diseases of the prostate include benign prostatic hyperplasia, prostatitis, prostatic intraepithelial neoplasia and cancer.

ADVANTAGE - The methods and reagents of the invention provide an early means of detecting diseases of the prostate and also provide new markers which can differentiate between the clinically important and unimportant prostate cancers without the use of surgery.

pp; 57 DwgNo 0/5

5/AB/14 (Item 2 from file: 351)
DIALOG(R)File 351:Derwent WPI

014359098
WPI Acc No: 2002-179799/200223
XRAM Acc No: C02-055908
Determining presence of specific nucleotide sequence in RNA reagent of sample by using a capture reagent having a label and a nucleotide sequence complementary to capture sequence attached to RNA reagent on microarray

Patent Assignee: GENISPHERE INC (GENI-N)
Inventor: GETTS R C; KADUSHIN J M
Number of Countries: 094 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200206511	A2	20020124	WO 2001US22818	A	20010719	200223	B

Priority Applications (No Type Date): US 2000219397 P 20000719
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200206511	A2	E	41	C12Q-000/00	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

Abstract (Basic): WO 200206511 A2
Abstract (Basic):

NOVELTY - Determining (M) presence of specific nucleotide sequence in an RNA reagent of target sample, which has a target nucleotide sequence and a capture sequence, involves utilizing a capture reagent (CR) having a first arm containing a label capable of emitting a detectable signal and at least one second arm having a nucleotide sequence complementary to a capture sequence attached to the RNA reagent on a microarray.

DETAILED DESCRIPTION - (M), comprises:

(1) incubating a mixture comprising a first component (C1) including an RNA reagent extracted directly from a target sample, which has a target nucleotide sequence and a capture sequence, and a second component (C2) comprising CR having a nucleotide sequence complementary to the capture sequence of the RNA reagent of C1, at a temperature (T1) and for a time sufficient to induce the capture sequence of the RNA reagent of C1 to bind to the complementary nucleotide sequence of the capture reagent of C2, and to form a pre-hybridized RNA-capture reagent complex, comprising the target nucleotide sequence;

(2) contacting the complex with a microarray having several features each containing a particular probe nucleotide sequence; and

(3) incubating the complex on the microarray at a temperature (T2) and for a time sufficient to hybridize the target nucleotide sequence of the pre-hybridized RNA-capture reagent complex to the complementary probe nucleotide sequence contained within the feature, where the presence of such hybridization results in the emission of the detectable signal from the corresponding feature, and its absence results in no emission of the detectable signal from the corresponding feature, thus generating a detectable hybridization pattern for subsequent analysis.

USE - (M) is useful for detecting presence of specific nucleotide sequence in an RNA reagent of a target sample (claimed). (M) is useful in a range of genomic applications such as gene expression profiling and high-throughput functional genomic analysis, and in differential gene expression assays, e.g. in analysis of diseased and normal tissue, e.g. neoplastic and normal tissue, different tissue or sub-tissue types.

ADVANTAGE - The method does not require the time- and labor-consuming enzymatic conversion of sample into a complementary copy, and significantly reduces the time and labor that are typically required to process and assay the nucleic acid target molecule for obtaining information about the genetic profile of the target nucleic acid sample and the source from which the sample was obtained. Nucleic

acid can be prepared in a shorter period of time.
pp; 41 DwgNo 0/2

5/AB/15 (Item 3 from file: 351)
DIALOG(R)File 351:Derwent WPI

014190105
WPI Acc No: 2002-010802/200201
XRAM Acc No: C02-002659
Haplotyping comprises separately analyzing first and second alleles of first and second single nucleotide polymorphisms of two different polymorphic loci, and determining haplotype based on each allele identification
Patent Assignee: POLYGENYX INC (POLY-N)
Inventor: LANDERS J E
Number of Countries: 094 Number of Patents: 002
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200175163	A2	20011011	WO 2001US10173	A	20010330	200201	B
AU 200149617	A	20011015	AU 200149617	A	20010330	200209	

Priority Applications (No Type Date): US 2000194425 P 20000404
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200175163	A2	E	77	C12Q-001/68	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

AU 200149617	A		C12Q-001/68	Based on patent WO 200175163

Abstract (Basic): WO 200175163 A2
Abstract (Basic):
NOVELTY - Haplotyping comprises analyzing first and second alleles of a first single nucleotide polymorphism (SNP1) of a first polymorphic locus (PL1) by specifically capturing the nucleic acid sample (NS) on a surface, separately analyzing a second SNP (SNP2) of a polymorphic locus of NS to identify both alleles of SNP2, and determining the haplotype based on the identification of each allele of each SNP.
DETAILED DESCRIPTION - The method involves analyzing a first polymorphic locus (PL1) of a nucleic acid within a sample by specifically capturing the nucleic acid on a surface and identifying a first allele (A1) of a first single nucleotide polymorphism (SNP1) of PL1, identifying a second allele (A2) of SNP1 of PL1 by specifically capturing the nucleic acid on a surface, separately analyzing a second SNP (SNP2) of a polymorphic locus of NS to identify both alleles of SNP2, and determining the haplotype based on the identification of each allele of each SNP.
The method optionally involves (M1) analyzing a genotype of SNP1 of a polymorphic locus of a nucleic acid within a sample in solution by detecting the presence or absence of a first labeled probe which specifically identifies a first putative allele of the SNP and detecting the presence or absence of a second labeled probe which specifically identifies a second putative allele of the SNP, separating NS based on the genotype of the first SNP, analyzing a second SNP of the polymorphic locus of the separated nucleic acid samples to identify the haplotype of the nucleic acid. The analysis of SNP1 is performed

using fluorescence detection. NS is separated using a flow cytometry. SNP2 is identified using a capture reaction.

An INDEPENDENT CLAIM is also included for a kit comprising one or more containers housing, a first set of allele specific oligonucleotides (ASOs) representing two ASOs, each containing one of the two alleles of a first SNP in a polymorphic locus, a second set of ASOs representing two ASOs, each containing one of the two alleles of a second SNP in a polymorphic locus, instructions for performing a hybridization reaction to determine a haplotype from a genomic DNA sample using the first and second sets of ASOs.

USE - The method is useful for haplotyping a nucleic acid within a sample (claimed). The method is useful for screening DNA to identify polymorphic haplotypes, and identification of haplotypes associated with predisposition to diseases as well as other genetically associated traits. SNP haplotyping is useful in linkage disequilibrium studies for the analysis of complex traits to localized genes involved in diseases such as diabetes, multiple sclerosis and asthma, diagnostic analysis to determine the presence or absence of a predisposing disease haplotype or other trait, pharmacogenomic analysis to identify haplotypes that correlates with either positive or negative responses to drugs and development, genome-wide scan studies for complex trait analysis using SNP haplotypes, instead of single SNPs to increase the statistical power. The haplotyping methods are useful for identifying both normal phenotypes and disease phenotypes. The methods are useful for identifying traits such as eye color and for diagnostics to determine presence or absence of predisposing disease haplotype in a subject. Such diseases include colon, breast cancer, cystic fibrosis, neurofibromatosis type 2, thalassemia, phenylketonuria, etc. Identification of haplotypes associated with phenotypic traits is useful for identifying predisposition to disease. The methods are also useful in prenatal screening to identify whether a fetus is afflicted with or is predisposed to develop a serious disease. Additionally, this information is useful for screening animals or plants bred for enhancing or exhibiting desired characteristics.

ADVANTAGE - SNP haplotype analysis is much more informative than single SNP loci analysis because it enables analysis of complex traits. The method is capable of assessing multiple allele in large number of genomic samples. The polymorphic loci can be used to define a new locus with a heterozygosity and informativeness significantly beyond that of any single marker contained. The high throughput method of SNP haplotyping provides improved methods for SNP haplotyping that can dramatically increase the rate of haplotype analysis and enables large scale haplotyping studies. The method is amenable to high throughput and allows the simultaneous discrimination haplotyping of multiple SNP loci for both chromosomes of an individual. Method can be performed on many nucleic acid samples at a time, thus providing massive quantities of haplotype information which is useful in characterizing complex traits and diseases. The method also provides fewer false readings.

pp; 77 DwgNo 0/6

5/AB/16 (Item 4 from file: 351)
DIALOG(R)File 351:Derwent WPI

014038390
WPI Acc No: 2001-522603/200157
XRAM Acc No: C01-156061
XRPX Acc No: N01-387272

Novel homogenous method for detecting polynucleotides by using an oligonucleotide probe labeled with an environment sensitive label , the

signal of which varies upon hybridization of probe with target polynucleotide
Patent Assignee: NURMI J (NURM-I)
Inventor: NURMI J
Number of Countries: 021 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200161034	A1	20010823	WO 2001FI128	A	20010213	200157	B

Priority Applications (No Type Date): FI 2000333 A 20000216
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200161034	A1	E	45	C12Q-001/68	

Designated States (National): JP US
Designated States (Regional): AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR

Abstract (Basic): WO 200161034 A1
Abstract (Basic):

NOVELTY - Homogenous detection of a target polynucleotide (tPN) in a sample, comprising contacting sample of PN, PN forming nucleic acids or their derivatives, with labeled oligonucleotide probe (OP) which hybridizes to tPN, where the label signal increases or decreases upon hybridization between them, exciting the label and measuring signal intensity by time resolved fluorometry to detect tPN, is new.

USE - For detecting a target polynucleotide, including a single or double stranded DNA or RNA or their derivatives, a hybrid of DNA and RNA or of DNA or RNA and a nucleic acid derivative such as peptide nucleic acid in a sample (claimed).

ADVANTAGE - The labels do not need any counteracting labels to distinguish the signals from a hybridized and a non-hybridized probe. The labels are stable with a long decay time and are sensitive to immediate chemical environment. Unlike, conventional TaqMan 5'-exonuclease assays, this assay does not require a quencher moiety in the probe. Measurements are carried out in a time-resolved manner and this label technology can easily be combined with conventional, prompt labels to make a multiplex assay without the need to rely on any spectral resolution software.

pp; 45 DwgNo 0/8

5/AB/17 (Item 5 from file: 351)
DIALOG(R)File 351:Derwent WPI

013205699
WPI Acc No: 2000-377572/200033
XRAM Acc No: C00-114448
In situ hybridization, useful e.g. for research and clinical diagnosis, uses probe modified with a labeled dendrimer to provide signal amplification
Patent Assignee: CHROMBIOS GMBH GES MOLEKULARE ZYTOGENETI (CHRO-N); METABION GMBH GES ANGEWANDTE BIOTECHNOLO (META-N); CHROMBIOS GMBH (CHRO-N)
Inventor: BICHLMAIER R; KOFLER A; STOECKL L
Number of Countries: 090 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
DE 19855180	A1	20000531	DE 1055180	A	19981130	200033	B
WO 200032810	A1	20000608	WO 99EP9148	A	19991125	200033	
AU 200013868	A	20000619	AU 200013868	A	19991125	200044	

Priority Applications (No Type Date): DE 1055180 A 19981130
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
DE 19855180	A1		10	C12Q-001/68	
WO 200032810	A1	G		C12Q-001/68	

Designated States (National): AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW

AU 200013868	A		C12Q-001/68	Based on patent WO 200032810

Abstract (Basic): DE 19855180 A1
Abstract (Basic):

NOVELTY - An in situ hybridization method is new and comprises at least one probe (I) comprising at least one dendrimer carrying at least one label (II).

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for a kit for this method comprising (I) and optionally also further reagents for cytogenetics and instructions for use.

USE - In situ hybridization is used for biological research and medical diagnosis, particularly in molecular genetics and histology, e.g. to test human, animal or plant samples, or mitotic, meiotic or interphase cells.

ADVANTAGE - The dendrimer-based probes provide amplification of the detection signal (by more than expected simply from the increased number of labels); provide control over incorporation of labels (so that the degree of signal amplification may be adjusted as required); and allow a single probe to be labeled simultaneously with different markers (so that 'ratio labeling' can be performed, simplifying four-color fluorescent microscopy since fewer filters are required for a given number of dyes). Also the cost of preparing probes is reduced.

pp; 10 DwgNo 0/1

5/AB/18 (Item 6 from file: 351)
DIALOG(R)File 351:Derwent WPI

008736826
WPI Acc No: 1991-240842/199133
XRAM Acc No: C91-104554
Quantitative assay method for suspect nucleic acid sequence - using chemically modified DNA or RNA molecular genetic probes
Patent Assignee: ORGENICS LTD (ORGE-N)
Number of Countries: 001 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
IL 96357	A	19910730	IL 96357	A	19840926	199133	B

Priority Applications (No Type Date): IL 96357 A 19840926; IL 73077 A 19840926

Abstract (Basic): IL 96357 A

A method for assaying for the presence or quantity of a suspect nucleic acid sequence of at least ten bases in a suspect sample contg. single stranded DNA or RNA , comprises: (a) contacting suspect sample with a molecular genetic probe comprising a modified nucleic acid sequence contg. complementary single stranded DNA or RNA

hybridisable with the suspect nucleic acid sequence, to form a hybridised complex, said modified nucleic acid sequence having been formed by alkylation, sulphonation, nitrosonation, or nitrophenylation; (b) removing non- hybridised nucleic acids to form a first reaction mixt. consisting essentially of the hybridised complex; (c) contacting the first reaction mixt. with antibodies specific to the modified portion of the modified nucleic acid sequence of said molecular genetic probe to form an antibody bound complex; (d) adding a labelling agent adapted to signal the presence of said antibodies; and (e) removing unreacted labelled antibody to form a second reaction mixt. which is essentially free of unreacted labelled antibody; (f) measuring the second reaction mixt. for the presence and/or extent of the presence of the labelled antibodies as an indication of the extent or presence of the suspect nucleic acid sequence in the sample

5/AB/19 (Item 7 from file: 351)
DIALOG(R)File 351:Derwent WPI

007748286
WPI Acc No: 1989-013398/198902
XRAM Acc No: C89-006161
XRPX Acc No: N89-010201
Identifying nucleic acid sequence - by binding prim. probe contg. sequence complementary to nucleic acid sequence and labelling substance and detecting signal
Patent Assignee: AISIN SEIKI KK (AISE); IND RES INST OF JAPAN (KOGY)
Number of Countries: 001 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
JP 63290962	A	19881128	JP 87125277	A	19870522	198902	B

Priority Applications (No Type Date): JP 87125277 A 19870522
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
JP 63290962	A		5		

Abstract (Basic): JP 63290962 A

Method comprises in detecting a given nucleic acid sequence by hybridisation between DNA - DNA , RNA - RNA or DNA - RNA , binding prim. probe contg. sequence complementary to object nucleic acid sequence or its part, or sec. probe bindable specifically with the prim. probe and a labelling substance capable of giving self signal display by Feulgen reaction and detecting the signal from the labelling substance to identify qualitatively or quantitatively the presence of required nucleic acid sequence.

The labelling substance is pref. basic dye such as fluorescent dye. The fluorescent dye is e.g. Acridine Yellow or acroflavin (3,6-diamino-10-methyl -acridinium chloride/3,6-acridineamine). The detection of the signal from the fluorescent dye is carried out by a fluorescent microscope or a fluorescent microscope equipped with a photomultiplier. Specific binding of the prim. probe and the sec. probe is based on hybridisation of mutually complementary single stranded oligomers.

USE/ADVANTAGE - The method is useful for detecting and identifying gene, esp. for detecting a given nucleic acid sequence. The method has high detecting sensitivity and can detect less than about 1 ng.DNA even 10 power -19 g/DNA by the use of fluorescent microscope equipped with a photomultiplier

5/AB/20 (Item 8 from file: 351)
DIALOG(R)File 351:Derwent WPI

007552319
WPI Acc No: 1988-186251/198827
XRAM Acc No: C88-083121
XRPX Acc No: N88-142243
Method of identifying configuration of nucleic acid - comprises e.g. binding primary probe contg. object nucleic configuration with labelling substance and detecting signal
Patent Assignee: AISIN SEIKI KK (AISE); IND RES INST OF JAPAN (KOGY)
Number of Countries: 001 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
JP 63122956	A	19880526	JP 86268557	A	19861113	198827	B

Priority Applications (No Type Date): JP 86268557 A 19861113
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
JP 63122956	A		5		

Abstract (Basic): JP 63122956 A

A method of identifying qualitatively or quantitavely given nucleic acid configuration comprises detecting it by hybridisation between DNA - DNA , RNA - RNA or DNA - RNA .

Process comprises binding a primary probe contg. object nucleic configuration or complementary configuration in part of the nucleic acid configuration. or a secondary probe consisting of a substance other than DNA and capable of binding specifically with the primary probe, and a labelling substance. The probe and labelling substance are bound by a non-covalent bond, and the presence of object nucleic acid configuration is identified qualitatively or quantitatively by detecting a signal from the labelling substance.

USE/ADVANTAGE - The method is useful for detecting a given nucleic acid configuration for the detection and identification of gene. Very high sensitivity is obtd., when a fluorescent dye is used as the labelling substance and detected by a fluorescent microscope. DNA of an extremely slight amt. (less than 1 pg.) can be detected by using a photomultiplier

5/AB/21 (Item 9 from file: 351)
DIALOG(R)File 351:Derwent WPI

007471198
WPI Acc No: 1988-105132/198815
XRAM Acc No: C88-047237
XRPX Acc No: N88-079733
Monoclonal antibodies to DNA - RNA hybrid complexes - used for determining the presence of a specific nucleic acid sequence
Patent Assignee: UNIV HAWAII (UYHA-N)
Inventor: FRANK M B; STUART W D
Number of Countries: 001 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
US 4732847	A	19880322	US 82454317	A	19821229	198815	B

Priority Applications (No Type Date): US 81271769 A 19810609; US 82454317 A 19821229; US 88155359 A 19880212
Patent Details:
Patent No Kind Lan Pg Main IPC Filing Notes
US 4732847 A 5

Abstract (Basic): US 4732847 A

IgM or IgG mouse monoclonal antibodies (MAbs) which specifically bind to DNA-RNA hybrid complexes but which do not bind to isolated RNA or DNA are claimed.

Also claimed is a method for detecting the presence of a nucleic acid sequence which comprises (a) fixing a DNA or RNA sequence to a solid support as a single strand, (b) hybridising the fixed single stranded nucleic acid sequence with a sequence of the other type of nucleic acid having a predetermined nucleic acid sequence to bind to any homologous fixed sequence to form a hybrid duplex, (c) adding to the hybrid duplex mouse IgG or IgM MAbs which specifically bind to DNA - RNA hybrid complexes and (d) determining the presence of MAb bound to the solid support by means of a label providing a detectable signal , the label being bound directly or indirectly to the MAb.

USE/ADVANTAGE - The method provides an accurate and simple technique for detecting the presence of a particular nucleic acid sequence by hybridisation in situ. The use of MAbs precludes significant binding to single stranded nucleic acids. The method can be used for e.g., detection of genes, structural, regulatory or expressing RNA or the presence of mutations. It can be used in hybrid DNA technology, disease diagnosis, gene identification or DNA and RNA isolation.

0/0

5/AB/22 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0271692 DBA Accession No.: 2001-10916 PATENT
Non-separation heterogenous assay for detecting, identifying, and measuring the concentration and activity of biological substances - hybridization assay for e.g. RNA or DNA or oligonucleotide determination
AUTHOR: Bauer-Moore A
CORPORATE SOURCE: Mississauga, Ontario, Canada.
PATENT ASSIGNEE: Gan Z 2001
PATENT NUMBER: WO 200125788 PATENT DATE: 20010412 WPI ACCESSION NO.: 2001-328366 (2034)
PRIORITY APPLIC. NO.: CA 2286414 APPLIC. DATE: 19991004
NATIONAL APPLIC. NO.: WO 2000CA1153 APPLIC. DATE: 20001003
LANGUAGE: English
ABSTRACT: A system (I) for measuring a biological substance using competitive binding between biological substances is claimed. The system comprises a vessel coated with reactant 1m a known amount of a labeled reactant 3 and an unknown amount of reactant 2. The reactions of the reactants cause a change of the label signal of reactant 3, which is directly proportional to the amount of reactant 2. Also claimed are: detecting the biological activity of a biological substance using the degradation of a substrate; and detecting the amount of an inhibitor to a biological substance. The method is used to measure the amount of a biological substance, particularly an inhibitor, in a sample, and for detecting biological activity of a biological substance. The method is simple and the signal formed can be measured directly. Reactant 1 is ss DNA, reactant 2 is DNA containing a

complementary sequence of ss DNA and reactant 3 is the labeled complementary ss DNA. Alternatively, reactant 2 is an enzyme, and reactant 1 is a substrate for it e.g. DNA, RNA, protein, PEG, oligosaccharide, oligonucleotide, etc. (18pp)

5/AB/23 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0260214 DBA Accession No.: 2000-14704 PATENT
Nucleic acid probe used in clinical diagnosis comprising labelled single-stranded nucleic acids complementary to specific nucleic acid sequences - a DNA probe involving antisense oligonucleotide
AUTHOR: Horie R; Ishiguro T; Tokunaga T; Yamamoto T; Saitoh J; Taya T
CORPORATE SOURCE: Yamaguchi-ken, Japan.
PATENT ASSIGNEE: Tosoh 2000
PATENT NUMBER: EP 1035214 PATENT DATE: 20000913 WPI ACCESSION NO.: 2000-566927 (2053)
PRIORITY APPLIC. NO.: JP 9958251 APPLIC. DATE: 19990305
NATIONAL APPLIC. NO.: EP 2000104448 APPLIC. DATE: 20000306
LANGUAGE: English
ABSTRACT: DNA probe comprising a single-stranded nucleic acid complementary to a specific sequence and labelled to give a measurable fluorescent signal on hybridization with the specific sequence, is claimed. Also claimed is a method of assaying a target nucleic acid containing a specific base sequence comprising amplifying the target nucleic acid in the presence of a single-stranded DNA probe complementary to the specific sequence, which is labelled to give off a measurable signal on hybridization with a nucleic acid containing the amplified target nucleic acid with DNA probe during and/or after the amplification. The 3' end of the nucleic acid probe is modified to contain (I). The DNA probe is useful in clinical diagnosis (e.g. gene diagnosis), and in the exploration of unknown genes. The DNA probe can also be used in quantitative or qualitative assays of DNA or RNA containing a specific nucleic acid sequence. The DNA probe does not undergo DNA elongation from the 3' end during amplification. (15pp)

5/AB/24 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0256210 DBA Accession No.: 2000-10700 PATENT
In situ hybridization, useful e.g. for research and clinical diagnosis, uses probe modified with a label dendrimer to provide signal amplification - the use of in situ hybridization
AUTHOR: Kofler A; Bichlmaier R; Stockl L
CORPORATE SOURCE: Planegg, Germany.
PATENT ASSIGNEE: Metabion; ChromBio 2000
PATENT NUMBER: DE 19855180 PATENT DATE: 20000531 WPI ACCESSION NO.: 2000-377572 (2033)
PRIORITY APPLIC. NO.: DE 1055180 APPLIC. DATE: 19981130
NATIONAL APPLIC. NO.: DE 1055180 APPLIC. DATE: 19981130
LANGUAGE: German
ABSTRACT: An in situ hybridization method is new and comprises at least one probe (DNA , RNA or peptide nucleic acid) (I) containing at least one dendrimer carrying at least one or more of both hapten and fluorescent labels (II). (I) is a chromosome paint or is a centromere-specific probe or probe for gene identification . (I) are

produced using dendrimer modified primers, particularly by polymerase chain reaction for extension of primers or by random priming. The sample for hybridization is a chromosome, cell nucleus, DNA spread or tissue sample and is tested by the primed in situ (PRINS) method, using different labeled dendrimers or different nucleic acid probes. Also claimed is a kit for this method comprising (I) and optionally suitable cytogenetics reagents including dextran sulfate or reagent for determining the labels, e.g. antibodies and instructions for use. The kit may include many different probes. In situ hybridization is used for biological research and medical diagnosis, e.g. in molecular genetics and histology, e.g. to test human, animal or plant samples, or mitotic, meiotic or interphase cells. (10pp)

5/AB/25 (Item 4 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0206327 DBA Accession No.: 97-01448 PATENT
Specific binding assay using signal-altering reagent - DNA probe homogeneous hybridization for e.g. diagnostic applications
AUTHOR: Becker M; Nelson N C
CORPORATE SOURCE: San Diego, CA, USA.
PATENT ASSIGNEE: Gen-Probe 1996
PATENT NUMBER: EP 747706 PATENT DATE: 961211 WPI ACCESSION NO.: 97-023324 (9703)
PRIORITY APPLIC. NO.: US 478221 APPLIC. DATE: 950607
NATIONAL APPLIC. NO.: EP 96108880 APPLIC. DATE: 960603
LANGUAGE: English
ABSTRACT: A new method for assaying for an analyte (e.g. a specific DNA or RNA fragment) in a sample involves: exposing the sample to a labeled binding partner (e.g. a DNA probe), with an analyte binding region and a label , where signal production from the label is preferentially protected from alteration by a signal altering ligand when the partner is bound to the analyte; treating with the ligand; and detecting the signal from unaltered label. The assay may be performed without separating bound and unbound probe, and at a constant temp., e.g. RT. Light absorbance or emission may be detected as the signal. The ligand may be tetrahydrothiophene, propanethiol, benzylmercaptan, sulfite, glycol sulfite, hydrosulfite, metabisulfite, thiosulfate, thiophosphate, metaarsenite, tellurite, arsenite or thiocyanate. The method may be used in homogeneous hybridization in e.g. diagnostic applications, and is versatile, since signal alteration may be effected under a wide range of conditions at constant temp., with high sensitivity. (37pp)

5/AB/26 (Item 5 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0170330 DBA Accession No.: 94-12881 PATENT
Detecting spatial relation between mRNA and gene in nucleus - fluorescence in situ hybridization 2-label method for low-abundance mRNA detection
PATENT ASSIGNEE: Univ.Massachusetts 1994
PATENT NUMBER: EP 612851 PATENT DATE: 940831 WPI ACCESSION NO.: 94-265968 (9433)
PRIORITY APPLIC. NO.: US 23953 APPLIC. DATE: 930226
NATIONAL APPLIC. NO.: EP 94610009 APPLIC. DATE: 940214
LANGUAGE: English
ABSTRACT: A new in situ hybridization method for detecting a specific

mRNA in spatial correlation with a corresponding gene involves: hybridization of nuclear RNA to an mRNA-specific DNA probe tagged with a 1st label, in non- DNA -denaturing conditions; generating a signal from the label; fixing the cell, so that the 1st signal is maintained at the site of transcription of the mRNA in the form of a focus or track of fluorescence; hybridizing the gene to a DNA -specific probe tagged with a 2nd label under DNA -denaturing conditions; generating a signal from the 2nd label ; and detecting 1st and 2nd signals as an indication of the spatial correlation of the mRNA to the gene. A single-label method is also claimed. The methods may be used to visualize intranuclear distribution of mRNA produced by expression of a specific gene, to compare expression levels of specific alleles of a gene, to determine whether viral infections are latent or productive, and to detect and quantify expression of exogenous genes. The methods increase the sensitivity and stability of in situ hybridization so that labile low-abundance mRNAs may be detected in the nucleus. (16pp)

5/AB/27 (Item 6 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0125114 DBA Accession No.: 91-12756 PATENT
Chemically modified DNA or RNA molecular probes and a method for testing for the presence or quantity of a nucleic acid utilizing them - DNA probe, RNA probe
PATENT ASSIGNEE: Orgenics 1991
PATENT NUMBER: IL 96357 PATENT DATE: 910630 WPI ACCESSION NO.: 91-240842 (9133)
PRIORITY APPLIC. NO.: IL 96357 APPLIC. DATE: 840926
NATIONAL APPLIC. NO.: IL 96357 APPLIC. DATE: 840926
LANGUAGE: English
ABSTRACT: A method for assaying for the presence or quantity of a suspect nucleic acid (NA) sequence of at least 10 bases in a suspect sample containing single-stranded DNA or RNA comprises: (a) contacting the suspect sample with a genetic probe comprising a modified NA sequence containing complementary single-stranded DNA or RNA that can hybridize with the suspect NA sequence, the modified NA sequence having been formed by alkylation, sulfonation, nitrosonation or nitrophenylation; (b) removing non- hybridized NAs to form a reaction mixture consisting essentially of the hybridized complex; (c) contacting the reaction mixture with antibodies specific to the modified portion of the modified NA sequence of the molecular genetic probe to form an antibody bound complex; (d) adding a label adapted to signal the presence of the antibodies; and (e) removing unreacted labeled antibody to form a second reaction mixture which is essentially free of unreacted labeled antibody; and (f) measuring the second reaction mixture for the presence and/or extent of the presence of the labeled antibodies as an indication of the extent or presence of the suspect NA sequence in the sample.

5/AB/28 (Item 7 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0119050 DBA Accession No.: 91-06692 PATENT
Cyclodextrin label compounds - fluorescence, luminescence, dye or substrate label for DNA probe, RNA probe, DNA primer, etc., for DNA hybridization, DNA sequencing, etc.

PATENT ASSIGNEE: Kosak K M 1991
PATENT NUMBER: WO 9102040 PATENT DATE: 910221 WPI ACCESSION NO.: 91-073518 (9110)
PRIORITY APPLIC. NO.: US 389796 APPLIC. DATE: 890804
NATIONAL APPLIC. NO.: WO 90EP4375 APPLIC. DATE: 900803
LANGUAGE: English
ABSTRACT: A new method for production of a cyclodextrin (CD) tracer comprises: coupling of a CD molecule (CD, a CD derivative or a CD label) containing an inclusion compound (e.g. fluorophore, scintillator, chemiluminescent compound, dye or substrate) to a specific ligand, ligator DNA or RNA and a label (e.g. an antigen, antibody, biotin, avidin, streptavidin, lectin or receptor); separation of the labeled fragments by size; and detection of e.g. emitted light from e.g. fluorophore-labeled fragment by activating the inclusion complexes via an energy transfer reaction. The CD labels provide higher signal efficiency and versatility in label colors, while maintaining uniform chemical and physical properties. They may be used for e.g. high volume RNA or DNA sequencing, DNA probe or RNA probe labeling for RNA or DNA hybridization assays., in immunoassays and in catalysis or detoxification. (69pp)

5/AB/29 (Item 8 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0086953 DBA Accession No.: 89-04944 PATENT
Identification of nucleic acid sequence - by probe hybridization and fluorescent signal detection
PATENT ASSIGNEE: Ind.Res.Inst.Jap. 1988
PATENT NUMBER: JP 63290962 (Kokai) PATENT DATE: 881128
WPI ACCESSION NO.: 89-013398 (8902)
PRIORITY APPLIC. NO.: JP 87125277 APPLIC. DATE: 870522
NATIONAL APPLIC. NO.: JP 87125277 APPLIC. DATE: 870522
LANGUAGE: Japanese
ABSTRACT: A new method for identification of nucleic acid sequences involves hybridization between DNA - DNA , RNA - RNA or DNA - RNA using a probe, containing a sequence complementary to all or part of the desired sequence, another probe, capable of specific binding with the 1st probe, and a label capable of giving self signal display by the Feulgen reaction. The presence of the desired nucleic acid sequence may be identified quantitatively or qualitatively by detection of the signal from the label. The preferred labels include basic dyes such as fluorescent dye e.g. acridine yellow or acroflavin. Detection of the signal from the fluorescent dye is performed using a fluorescent microscope, optionally equipped with a photomultiplier. Specific binding of the 2 probes is based on hybridization of mutually complementary single-stranded oligomers. The new method can be used for detection and identification of genes, especially for detection of a given nucleic acid sequence. The method exhibits high sensitivity of detection and is capable of detecting less than 1 ng DNA , even 10 power -19 g/ DNA using a fluorescent microscope equipped with a photomultiplier. (5pp)

5/AB/30 (Item 9 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0079242 DBA Accession No.: 88-10091 PATENT
Method of identifying configuration of nucleic acid - comprises e.g.

binding primary probe containing object nucleic configuration with labeling substance and detecting signal
PATENT ASSIGNEE: Ind.Res.Inst.Jap. 1988
PATENT NUMBER: JP 63122956 (Kokai) PATENT DATE: 880526
WPI ACCESSION NO.: 88-186251 (8827)
PRIORITY APPLIC. NO.: JP 86268557 APPLIC. DATE: 861113
NATIONAL APPLIC. NO.: JP 86268557 APPLIC. DATE: 861113
LANGUAGE: Japanese
ABSTRACT: A method of identifying qualitatively or quantitatively a given nucleic acid configuration comprises detecting it by hybridization between DNA - DNA , DNA - RNA or RNA - RNA . The process comprises binding a primary probe containing the nucleic acid or its complementary nucleic acid , or a secondary probe consisting of a substance other than DNA and capable of binding specifically with the primary probe, and a labeling substance. The probe and labeling substance are bound by a non-covalent bond, and the presence of the object nucleic acid configuration is identified qualitatively or quantitatively by detecting a signal from the labeling substance. The method is useful for detecting a given nucleic acid configuration for the detection and identification of a gene. Very high sensitivity is obtained when a fluorescent dye is used as the label and detected using a fluorescence microscope. DNA in quantities less than 1 pg can be detected by using a photomultiplier. (5pp)
?ds

Set	Items	Description
S1	117574	(NA OR DNA OR NUCLEIC(W)ACID?) (S) (DETERM? OR DETN OR DETG OR ASSAY? OR IDENT?)(S)(RIBONUCLEIC(W)ACID? OR RNA)
S2	31744	S1 AND (HYBRID? OR CAPTUR?(4W)REAGENT? OR DENDRIMER?)
S3	27982	S1 (S)(HYBRID? OR CAPTUR?(3W)REAGENT? OR DENDRIMER?)
S4	55	S3 AND LABEL?(5W)SIGNAL?
S5	30	RD (unique items)
S6	5449	S3 AND GENE?(W)EXPRESSION?
S7	59804	(NA OR DNA OR NUCLEIC(W)ACID?)(S)DETECT?(S)(RNA OR RIBONUCLEIC(W)ACID?)
S8	22640	S7(S)(HYBRID? OR CAPTURE(3W)REAGENT? OR DENDRIMER? OR OLIGONUCLEOTIDE?)
S9	89	S8 AND LABEL?(5W)SIGNAL?
S10	50	RD (unique items)
S11	28	S10 NOT S5

?t11/3 ab/1-28
>>>No matching display code(s) found in file(s): 65, 342

11/AB/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10905353 20572541 PMID: 11121494
Double- labeled donor probe can enhance the signal of fluorescence resonance energy transfer (FRET) in detection of nucleic acid hybridization.
Okamura Y; Kondo S; Sase I; Suga T; Mise K; Furusawa I; Kawakami S; Watanabe Y
Laboratory of Molecular Biophotonics, 5000 Hirakuchi, Hamakita, Shizuoka 434-8555, Japan.
Nucleic acids research (ENGLAND) Dec 15 2000, 28 (24) pE107, ISSN 1362-4962 Journal Code: DF1
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
A set of fluorescently-labeled DNA probes that hybridize with the target RNA and produce fluorescence resonance energy transfer (FRET)

signals can be utilized for the detection of specific RNA . We have developed probe sets to detect and discriminate single-strand RNA molecules of plant viral genome, and sought a method to improve the FRET signals to handle in vivo applications. Consequently, we found that a double-labeled donor probe labeled with Bodipy dye yielded a remarkable increase in fluorescence intensity compared to a single-labeled donor probe used in an ordinary FRET. This double-labeled donor system can be easily applied to improve various FRET probes since the dependence upon sequence and label position in enhancement is not as strict. Furthermore this method could be applied to other nucleic acid substances, such as oligo RNA and phosphorothioate oligonucleotides (S-oligos) to enhance FRET signal. Although the double-labeled donor probes labeled with a variety of fluorophores had unexpected properties (strange UV-visible absorption spectra, decrease of intensity and decay of donor fluorescence) compared with single-labeled ones, they had no relation to FRET enhancement. This signal amplification mechanism cannot be explained simply based on our current results and knowledge of FRET. Yet it is possible to utilize this double-labeled donor system in various applications of FRET as a simple signal-enhancement method.

11/AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07917493 93354533 PMID: 8350985
Preferential expression of superoxide dismutase messenger RNA in melanized neurons in human mesencephalon.
Zhang P; Damier P; Hirsch EC; Agid Y; Ceballos-Picot I; Sinet PM; Nicole A; Laurent M; Javoy-Agid F
INSERM U289, Hopital de la Salpetriere, Paris, France.
Neuroscience (ENGLAND) Jul 1993, 55 (1) p167-75, ISSN 0306-4522 Journal Code: NZR
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
The copper-zinc-dependent superoxide dismutase messenger RNA expression was studied at cellular level by in situ hybridization , using a 35S-labelled complementary DNA probe homologous to human copper-zinc-dependent superoxide dismutase messenger RNA , in the dopaminergic neuron-containing areas of the human mesencephalon (the substantia nigra pars compacta, ventral tegmental area, central gray substance and peri- and retrorubral region corresponding to catecholaminergic cell group A8). The autoradiographic labelling signal was localized in neurons. No detectable hybridization signal could be found in the glial cells. Copper-zinc-dependent superoxide dismutase messenger RNA was detected in melanin-containing neurons as well as in non-melanized neurons. Quantification at cellular level, taking the autoradiographic silver grain density as an index of the abundance of copper-zinc-dependent superoxide dismutase messenger RNA , indicated that hybridization level was higher in the melanized than in the non-melanized neurons within a region. Among melanized neurons, cellular copper-zinc-dependent superoxide dismutase messenger RNA content was lowest in the neurons of the substantia nigra. No significant difference in levels of transcripts was evidenced between the groups of non-melanized neurons. The data suggest that the abundance of copper-zinc-dependent superoxide dismutase messenger RNA is higher in the mesencephalic neurons containing neuromelanin compared to other neurons. Thus, the melanized neurons have a particular defence system against oxygen toxicity, which may represent a basis for their preferential vulnerability to Parkinson's disease.

11/AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07534732 92030128 PMID: 1657053
The application of AmpliProbe in diagnostics.
Yang JQ; Tata PV; Park-Turkel HS; Waksal HW
ImClone Systems, Inc., New York, NY 10014.
BioTechniques (UNITED STATES) Sep 1991, 11 (3) p392-7, ISSN 0736-6205 Journal Code: AN3
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
AmpliProbe System is a rapid, enzyme-labeled, non-isotopic probe system that has high sensitivity and flexibility. AmpliProbe System consists of two major components: target-specific "primary" probes and target-independent, enzyme- labeled , signal -generating "secondary" probes. The visualization of the complemental hybridization between the target DNA or RNA and probes is accomplished by an enzymatic chemiluminescent reaction. The AmpliProbe System format allows hybridization and signal visualization to be completed within five to seven hours. In this paper we present several successful applications of AmpliProbe in the detection of infectious disease pathogens and the detection of gene amplification and transcription elevation in the evaluation of oncogenes in cancer research.

11/AB/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06829562 92201233 PMID: 1802706
Localization of U3 RNA molecules in nucleoli of HeLa and mouse 3T3 cells by high resolution in situ hybridization.
Puvion-Dutilleul F; Mazan S; Nicoloso M; Christensen ME; Bachellerie JP
Laboratoire de Biologie et Ultrastructure du Noyau, CNRS (UPR 272), Villejuif/France.
European journal of cell biology (GERMANY) Dec 1991, 56 (2) p178-86, ISSN 0171-9335 Journal Code: EM7
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
We have examined the ultrastructural localization of U3 RNA in the nucleoli of HeLa and mouse 3T3 cells by in situ hybridization with a biotinylated U3 DNA probe and subsequent detection of hybrids with electron microscopy by direct immunogold labeling . The highest levels of signal density for U3 RNA are detected over the dense fibrillar component (DFC) of the nucleolus, including the interfaces between DFC and the enclosed fibrillar center (FC) on the one hand and DFC and the granular component (GC) on the other hand. Lower but significant signals also are observed over GC, which indicate, taking into account the high relative volume of GC in a nucleolus, that a substantial fraction of U3 RNA is present in this compartment where the more mature forms of pre-rRNA accumulate. In parallel, the localization of fibrillarin was analyzed by immunogold detection , demonstrating that fibrillarin and U3 RNA have a roughly similar distribution, although quantitative measurements reveal that the signal ratio for both molecules exhibit significant differences among the major ultrastructural components of the nucleolus.

11/AB/5 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

13088415 BIOSIS NO.: 200100295564
Preparation of nonradioactive probes for in situ hybridization.
AUTHOR: Abraham Timothy W(a)
AUTHOR ADDRESS: (a)Ambion, Inc., 2130 Woodward Street, Austin, TX, 78744** USA
JOURNAL: Methods (Orlando) 23 (4):p297-302 April, 2001
MEDIUM: print
ISSN: 1046-2023
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: In situ hybridization (ISH) enables the precise localization of RNA targets and provides an avenue to study the temporal and spatial patterns of expression of specific genes. ISH has evolved from being an esoteric technique to one that is routinely used by researchers in many areas of research. A major driving force has been the development of numerous nonisotopic labeling and signal detection methods. Historically, radioactive probes and autoradiography provided sensitivity that was unattainable with non isotopic probes. But the long exposure times required for signal detection and the perceived dangers associated with radioactivity limit its use. Advances in nonisotopic detection systems have overcome many of the limitations associated with using radiolabeled probes. One of the most significant contributions from nonisotopic methods is the ability to discriminate between multiple nucleic acid sequences simultaneously.

2001

11/AB/6 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

08505383 Genuine Article#: 293RJ Number of References: 232
Title: Cytochemical nucleic acid research during the twentieth century
Author(s): vanderPloeg M (REPRINT)
Corporate Source: LEIDEN UNIV,MED CTR, DEPT MOL CELL BIOL, LAB CYTOCHEM & CYTOMETRY, WASSENAARSEWEG 72/NL-2333 AL LEIDEN//NETHERLANDS/ (REPRINT)
Journal: EUROPEAN JOURNAL OF HISTOCHEMISTRY, 2000, V44, N1, P7-42
ISSN: 1121-760X Publication date: 20000000
Publisher: LUIGI PONZIO E FIGLIO, VIA D DA CATALOGNA 1/3, 27100 PAVIA, ITALY
Language: English Document Type: ARTICLE

11/AB/7 (Item 1 from file: 50)
DIALOG(R)File 50:CAB Abstracts

03790233 CAB Accession Number: 990107277
Prolactin induces protamine 2 mRNA expression in rat testis.
Hondo, E.; Kobayashi, T.; Ishiguro, N.; Kurohmaru, M.; Kitamura, N.; Yamada, J.; Nagahama, Y.
Department of Veterinary Anatomy, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido 080-8555, Japan.
Journal of Reproduction and Development vol. 45 (3): p.205-212
Publication Year: 1999

ISSN: 0916-8818 --
Language: English
Document Type: Journal article
The effects of prolactin on transcription during spermatogenesis was examined by subtractive DNA hybridization and differential screening. A protamine 2 cDNA fragment was isolated from one of the genes up-regulated in testes of rats 6 h after prolactin injection. In situ hybridization to detect protamine 2 mRNA was performed using digoxigenin- labelled RNA probes. Weak signals were detected from preleptotene to early pachytene spermatocytes, elongated spermatids and spermatozoa; strong ones were detected in mid- to late-pachytene, diplotene, and secondary spermatocytes, and early round spermatids. Localization of protamine 2 mRNA coincided with that of prolactin receptor mRNA described previously. The time-dependent expression of protamine 2 mRNA was compared with that of LH receptor mRNA after prolactin administration, by northern blotting. Protamine 2 mRNA was up-regulated 1 h after prolactin treatment, and stable levels were maintained for another 13 h. LH receptor mRNA levels increased much later, at 13 h after prolactin injection. It is concluded that up-regulation of protamine 2 expression is independent of the LH pathway. 39 ref.

11/AB/8 (Item 1 from file: 65)
DIALOG(R)File 65:Inside Conferences

02281042 INSIDE CONFERENCE ITEM ID: CN023847380
Horseradish Peroxidase Labeled Oligonucleotides and Tyramide Signal Amplification for Sensitive DNA and RNA Detection by in Situ Hybridization
Raap, T.
CONFERENCE: Nucleic acid-based technologies: Europe-Annual meeting; 3rd
NUCLEIC ACID BASED TECHNOLOGIES EUROPE, 1997; 3rd P: 10:45
Newton Upper Falls, MA, Cambridge Healthtech Institute, (1997)
LANGUAGE: English DOCUMENT TYPE: Conference Preprints and programme
CONFERENCE SPONSOR: Cambridge healthtech Institute
CONFERENCE LOCATION: Lisbon
CONFERENCE DATE: Oct 1997 (199710) (199710)

11/AB/9 (Item 1 from file: 149)
DIALOG(R)File 149:TGG Health&Wellness DB(SM)

01721519 SUPPLIER NUMBER: 19825781 (USE FORMAT 7 OR 9 FOR FULL TEXT)
Localization of the ATP-sensitive K+ channel subunit Kir6.2 in mouse pancreas.
Suzuki, Masakazu; Fujikura, Keiko; Inagaki, Nobuya; Seino, Susumu; Takata, Kuniaki
Diabetes, v46, n9, p1440(5)
Sep,
1997
PUBLICATION FORMAT: Magazine/Journal; Refereed ISSN: 0012-1797
LANGUAGE: English RECORD TYPE: Fulltext TARGET AUDIENCE: Professional
WORD COUNT: 3651 LINE COUNT: 00303

11/AB/10 (Item 1 from file: 351)
DIALOG(R)File 351:Derwent WPI

014328788
WPI Acc No: 2002-149491/200220
XRAM Acc No: C02-046508
Detecting or quantifying a specific nucleic acid in a sample by hybridizing primers to the target nucleic acid, extending the primers and detecting extended primer by label detection or mass spectrometry
Patent Assignee: MORISAWA S (MORI-I); WANG X B (WANG-I); MORISAWA N (MORI-I)
Inventor: WANG X B
Number of Countries: 028 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
EP 1162278	A2	20011212	EP 2001304958	A	20010606	200220 B
CA 2349810	A1	20011208	CA 2349810	A	20010607	200220
JP 2002027993	A	20020129	JP 2001166477	A	20010601	200224

Priority Applications (No Type Date): US 2001862417 A 20010523; US 2000209987 P 20000608
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
EP 1162278	A2	E	10	C12Q-001/68	
Designated States (Regional): AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR					
CA 2349810	A1	E		C12Q-001/68	
JP 2002027993	A		12	C12N-015/09	

Abstract (Basic): EP 1162278 A2
Abstract (Basic):
NOVELTY - Detecting or quantifying a target nucleic acid in a sample comprises annealing primers to a specific position on the target nucleic acid, extending those primers using non-terminating and optionally terminating nucleotides which are optionally labeled, and detecting extended primer by label detection or mass spectrometry.
DETAILED DESCRIPTION - Detecting or quantifying a target nucleic acid in a sample, comprising;
(a) preparing primers specific to a position on the target;
(b) annealing the primers with the target under high stringency to form a duplex;
(c) mixing the duplex with 1,2 or 3 types of free non-terminator nucleotides and at least one non-terminator type optionally labeled with a detectable marker, and optionally a type of terminator nucleotide different from the non-terminator nucleotides;
(d) performing primer extension by enzymatic or chemical means; and
(e) detecting or quantifying the amount of labeling signal on the extended nucleotides; or
(f) detecting or quantifying the amount of extended primers by mass spectrometry.
USE - The method is used to detect and quantify specific nucleic acid.
ADVANTAGE - The method provides a faster, cheaper, more sensitive assay which produces less biohazard or radioisotope waste than prior art northern analysis and RNase protection assays.
pp; 10 DwgNo 0/2

11/AB/11 (Item 2 from file: 351)
DIALOG(R)File 351:Derwent WPI

014285426
WPI Acc No: 2002-106127/200214

XRAM Acc No: C02-032542
Novel vector comprising double stranded DNA having target sequence and chimeric molecule comprising sequence specific polyamide moiety bound non-covalently to target and ligand moiety covalently linked to polyamide
Patent Assignee: IST RICERCHE BIOL MOLECOLARE ANGELETTI (RICE-N)
Inventor: BIANCHI E; FATTORI D; INGALLINELLA P; KINZEL O; PESSI A
Number of Countries: 023 Number of Patents: 002
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200188160	A2	20011122	WO 2001IB980	A	20010511	200214	B
AU 200158708	A	20011126	AU 200158708	A	20010511	200222	

Priority Applications (No Type Date): GB 200011938 A 20000517
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200188160	A2	E	98	C12N-015/63	
	Designated States (National): AU CA JP US				
	Designated States (Regional): AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR				
AU 200158708	A			C12N-015/63	Based on patent WO 200188160

Abstract (Basic): WO 200188160 A2
Abstract (Basic):
NOVELTY - A vector (conjugate) (I) comprising a double-stranded DNA (dsDNA) (Ia) having at least one target sequence (T); and a chimeric molecule (Ib) which comprises (i) a sequence specific polyamide (SSP) moiety bound non-covalently to (T); and (ii) a ligand moiety (L) covalently linked to SSP, is new.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:
(1) a composition comprising (I) and a carrier;
(2) synthesis (M1) of SSP on a solid support involving:
(a) attaching an N-terminal of the polyamide to the solid support via a safety-catch linker, -S(=O)2-NH-; and
(b) following synthesis of the polyamide, removing it from the solid support by cleavage of the safety-catch linker by activation and nucleophilic attachment;
(3) introducing (M2) a dsDNA into a cell or a sub-cellular compartment involving:
(a) providing (Ib) which comprises SSP and (L) linked covalently to the SSP moiety, and capable of being directed to the cell or the sub-cellular compartment;
(b) providing a dsDNA which includes a target sequence for the SSP moiety, under conditions where (Ib) binds to the dsDNA to provide a vector; and
(c) bringing the vector into contact with the cell under conditions for uptake of the vector and transport of the dsDNA;
(4) a eukaryotic cell obtained by (M2); and
(5) progeny of a eukaryotic cell obtained by (M2).
ACTIVITY - Antibacterial; Virucide.
MECHANISM OF ACTION - Gene therapy; Vaccine.
No biological data given.
USE - (I) Is useful in a method of treatment of the human or animal body and for preparing a medicament for treating a condition treatable by gene therapy. (I) Is also useful in gene therapy techniques. (M2) is useful for introducing a dsDNA into the nucleus of a eukaryotic cell which involves providing (Ib) which comprises SSP and (L) linked covalently to SSP moiety and capable of being directed to the nucleus of the eukaryotic cell; providing a dsDNA which includes a target sequence for the SSP moiety, under conditions where (Ib) binds to the dsDNA provide a vector; and bringing the vector into contact with the

eukaryotic cell under conditions for uptake of the vector and transport of the dsDNA. The vector is brought into contact with the eukaryotic cell in vivo, ex vivo or in vitro. The eukaryotic cell is preferably a CHO cell (all claimed). (I) is also used to deliver DNA encoding antigens (viral antigens, bacterial antigens or host protein antigens) useful as vaccines.

pp; 98 DwgNo 0/4

11/AB/12 (Item 3 from file: 351)
DIALOG(R)File 351:Derwent WPI

014081980
WPI Acc No: 2001-566194/200164
XRAM Acc No: C01-168191

Detecting nucleic acid from genetically modified organisms, useful particularly for analysis of foods, based on hybridization of fragments to array of reference sequences

Patent Assignee: PAUL H (PAUL-I); SEIDEL B M (SEID-I)
Inventor: PAUL H; SEIDEL B M
Number of Countries: 001 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
DE 10003763	A1	20010809	DE 1003763	A	20000128	200164	B

Priority Applications (No Type Date): DE 1003763 A 20000128
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
DE 10003763	A1		6	C12Q-001/68	

Abstract (Basic): DE 10003763 A1
Abstract (Basic):

NOVELTY - Method for detecting DNA and/or RNA sequences (D) of at least one genetically modified organism in a sample. Many (D), of different lengths, are extracted from the sample, labeled with a characteristic signal (F) and applied to carrier unit on which are arranged many reference DNA sequences (R). Those sequences (H) that hybridize to R are selected and a measurement of H is made from the signal F.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for a device for the process consisting of a carrier for (R) and a unit for analyzing hybridized sequences (H).

USE - The method is used to detect genetically modified organisms (or derived products) in animal or plant foods (also in tobacco and cosmetics), to differentiate between types of animals and plants, to detect microorganisms and/or to determine type purity.

ADVANTAGE - The method can detect not only promoters, terminators, reporter or marker genes, but also the structural gene responsible for the genetic modification, and partially degraded DNA can be detected. The carrier unit may carry hundreds or thousands of R, so many different genetic modifications can be screened for on a single carrier, providing high throughput analysis. Compared with polymerase chain reaction, the method has higher resolution and better reliability, also it is less expensive and less time consuming.

DESCRIPTION OF DRAWING(S) - Diagram of the process. Nucleic acid segments (D) of a genetically modified organism, labeled with fluorophore (F), are tested for hybridization with array of reference sequences (R). Those (D), designated (H), that hybridize, and are retained after washing, are detected from the signal produced by F.

pp; 6 DwgNo 1/1

11/AB/13 (Item 4 from file: 351)
DIALOG(R)File 351:Derwent WPI

013966147
WPI Acc No: 2001-450361/200148
Related WPI Acc No: 2000-206023
XRAM Acc No: C01-135958
Analyzing a polynucleotide produced by amplifying cDNA or genomic DNA involves hybridizing terminus probes having constant and variable region to adapter-modified restriction fragment generated from the polynucleotide
Patent Assignee: PERKIN-ELMER CORP (PEKE)
Inventor: HUNKAPILLER M W; RICHARDS J H
Number of Countries: 001 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
US 6258539	B1	20010710	US 98135381	A	19980817	200148	B
			US 99303774	A	19990430		

Priority Applications (No Type Date): US 99303774 A 19990430; US 98135381 A 19980817
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
US 6258539	B1		19	C12Q-001/68	CIP of application US 98135381

Abstract (Basic): US 6258539 B1
Abstract (Basic):
NOVELTY - Analyzing a polynucleotide by forming restriction fragment (RF) having first, second terminus and a termini generated by restriction endonuclease (RE), from the polynucleotide, joining an adapter to a terminus of RF to produce adapter-modified RF (I) and hybridizing a terminus probe having constant and variable region to single strand of (I) at a position including the terminus generated by RE.

USE - Analyzing a polynucleotide which is a cDNA or genomic DNA, or which is produced by amplifying a portion of a cDNA preparation or a portion of genomic DNA preparation (claimed).

The method allows simultaneous analysis of multiple different polynucleotides of polynucleotide composition e.g., cDNA or genomic DNA libraries, and the isolation of polynucleotides of interest identified through the analytical techniques. The analysis of RNA populations has utilities in research, diagnosis or treatment of a variety of diseases. The base sequence information contained within identifier sequences can be used to detect , discover or compare polymorphic sequences, to develop oligonucleotide primers to isolate the polynucleotide from which a specific identifier sequence is derived.

Analysis of large complex populations of polynucleotides may be used to produce sufficient information about a polynucleotide population so that differences between polynucleotide populations may be ascertained. Thus fingerprints of a polynucleotide population may be compared with fingerprints of other complex polynucleotide populations.

ADVANTAGE - The method permits the simultaneous analysis of a large number of different mRNA molecules that form a given mRNA population. Multiple identifier sequences may be obtained in parallel, thus permitting the rapid characterization of the large number of polynucleotides.

DESCRIPTION OF DRAWING(S) - The figure shows the terminus probes

which hybridize to adapter-modified representative restriction fragments.
pp; 19 DwgNo 1A/7

11/AB/14 (Item 5 from file: 351)
DIALOG(R)File 351:Derwent WPI

013531451
WPI Acc No: 2001-015657/200102
XRAM Acc No: C01-004119
Detecting presence or absence of microbial target molecules electrophoretically, by using capture probes immobilized to electrophoretic matrix, that specifically bind to target molecule in test sample
Patent Assignee: MOSAIC TECHNOLOGIES (MOSA-N)
Inventor: BOLES T C
Number of Countries: 093 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200060120	A2	20001012	WO 2000US8773	A	20000331	200102	B
AU 200041898	A	20001023	AU 200041898	A	20000331	200107	
EP 1173613	A2	20020123	EP 2000921605	A	20000331	200214	
			WO 2000US8773	A	20000331		

Priority Applications (No Type Date): US 99286091 A 19990402
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200060120	A2	E	61	C12Q-001/68	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW

AU 200041898	A		C12Q-001/68	Based on patent WO 200060120
EP 1173613	A2	E	C12Q-001/68	Based on patent WO 200060120

Designated States (Regional): AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI

Abstract (Basic): WO 200060120 A2
Abstract (Basic):
NOVELTY - Detecting presence or absence of a microorganism by detecting presence or absence of microbiological target molecules (II), identifying a nucleotide sequence mutation site in a putative mutant target molecule, by electrophoresis, involves use of capture probes (I) immobilized to an electrophoretic medium which specifically bind to or are bound by specific target molecules.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following: (1) detecting (M1) presence or absence of microorganism (M) in test sample (S), involves introducing (II) into electrophoresis medium (EM) having (I), subjecting EM to electric field resulting in electrophoretic migration of (II) into a region of EM having immobilized (I), and detecting presence of (II) or (I)/(I) complexes immobilized in EM; (2) detecting (M2) presence or absence of (II) in (S) using an adapter molecule by forming an adapter/target hybridization complex by contacting (II) from (S) under conditions suitable for hybridization with an adapter polynucleotide, thus forming an adapter/hybridization complex, which is introduced into EM containing (I) Immobilized within a region of EM that is subjected to

an electric field resulting in the electrophoretic migration of the adapter/target complex into a region of EM containing immobilized (I) and then detecting the presence of adapter/target/(I) complexes immobilized in the medium; (3) detecting (M3) presence or absence of microorganism by detecting presence or absence of (II) in a test sample using a signal polynucleotide displacement reaction involves forming (I)/signal polynucleotide sequence (I) comprising the nucleotide sequence that is complementary to a region of (II), with at least one signal polynucleotide comprising a nucleotide sequence that is partially homologous to (II) nucleotide sequence region used to hybridize with (I), under conditions suitable for hybridization between (I) and signal polynucleotide, thereby forming (I)/signal polynucleotide complex, introducing (II) into EM comprising (I) immobilized on it, subjecting EM to an electric field resulting in the electrophoretic migration of (II) into a region of EM containing immobilized (I) and then detecting the presence of at least one liberated signal polynucleotide in the signal layer within the medium, thus indicating the presence of (II) in (S); (4) identifying (M4) a nucleotide sequence mutation site in a putative mutant target molecule present in (S) involves introducing the putative mutant target molecules into EM, subjecting the EM to an electric field resulting in the electrophoretic migration of putative mutant target molecules into a region of EM containing immobilized (I) and then detecting the presence of the mutant target molecule/(I) complexes immobilized within the medium; (5) detecting (M5) presence or absence of microbial target molecule in (S) using a displacement assay involves introducing the target molecules into EM comprising (I) complexes (comprising labeled signal nucleic acid molecule hybridized with a tether nucleic acid molecule) immobilized within the medium, subjecting EM to an electric field resulting in the electrophoretic migration of microbial target molecules into a region of EM containing immobilized (I), forming a new hybrid complex by contacting the target molecule with (I) complex, in which the signal nucleic acid molecule is displaced by the target molecule, thus forming a new hybrid complex comprising the target molecule hybridized with tether nucleic acid molecule and then detecting the signal nucleic molecule which indicates the presence of a target molecule in (S); and (6) detecting (M6) the presence of a microbial target molecule in (S) using a reverse displacement assay involves introducing the target molecules into EM comprising (I) complexes (comprising labeled signal nucleic acid molecule hybridized with a tether nucleic acid molecule) immobilized within the medium, subjecting EM to an electric field resulting in the electrophoretic migration of microbial target molecules into a region of EM containing immobilized (I), forming a target-signal hybrid complex by contacting the target molecule with (I) complex, in which the signal nucleic acid molecule is displaced by, and hybridizes with, the target molecule, thus forming a target-signal hybrid complex and then detecting the target-signal hybrid complex which indicates the presence of a target molecule in (S).

USE - The method is useful for identifying bacteria Serratia marcescens, Staphylococcus epidermidis, Staphylococcus aureus, Escherichia coli, Bacillus cereus, Enterobacter cloacae, Streptococcus pyogenes, Staphylococcus warneri, Streptococcus(alpha-hemolytic), Streptococcus mitis, Salmonella, Serratia liquifaciens, Klebsiella, Propionibacterium acnes, Yersinia enterocolitica, Pseudomonas fluorescens, Pseudomonas putida in blood, plasma, platelets, erythrocytes, urine, feces, sweat, tracheal exudate, aqueous humor, vitreous humor, skin, hair, cell, tissue and organ culture systems (claimed).

ADVANTAGE - The methods are fast, sensitive, efficient and enable a accurate electrophoretic analysis of potentially contaminating

microorganisms in a test sample using immobilized capture probes that specifically bind to a microbial target molecule in presence of a microorganism. The sensitivity of the detection allows for detecting microorganisms using a non-radioactive means and thus provides safer and convenience methods for detecting contaminating microorganisms DESCRIPTION OF DRAWING(S) - The figure shows the different stages involved in detecting bacterial target molecules.
pp; 61 DwgNo 1/10

11/AB/15 (Item 6 from file: 351)
DIALOG(R)File 351:Derwent WPI

011763185
WPI Acc No: 1998-180095/199817
XRAM Acc No: C98-057913
XRPX Acc No: N98-142462
New heterocyclic nucleoside or nucleotide analogues - containing reporter groups, useful as stable labelling agents for nucleic acid detection and sequencing
Patent Assignee: BOEHRINGER MANNHEIM GMBH (BOEF); ROCHE DIAGNOSTICS GMBH (HOFF)
Inventor: MUEHLEGGER K; VAN DER ELTZ H; VON DER ELTZ H
Number of Countries: 021 Number of Patents: 004
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
DE 19637042	A1	19980319	DE 1037042	A	19960912	199817	B
WO 9811104	A1	19980319	WO 97EP4972	A	19970911	199818	
EP 927180	A1	19990707	EP 97909251	A	19970911	199931	
			WO 97EP4972	A	19970911		
JP 2001502665	W	20010227	WO 97EP4972	A	19970911	200115	
			JP 98513261	A	19970911		

Priority Applications (No Type Date): DE 1037042 A 19960912
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
DE 19637042	A1		8	C07D-405/04	
WO 9811104	A1	G	30	C07D-405/04	
Designated States (National): CA JP US					
Designated States (Regional): AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
EP 927180	A1	G		C07D-405/04	Based on patent WO 9811104
Designated States (Regional): AT BE CH DE DK ES FR GB IE IT LI NL SE					
JP 2001502665	W		24	C07D-405/04	Based on patent WO 9811104

Abstract (Basic): DE 19637042 A
Heterocyclic (e.g. pyrrole, pyrazine or oxazine derivative) nucleoside or nucleotide analogues of formula (I) and their tautomers and salts are new.
R1,R2 = H, O, halo, OH, optionally substituted thio, optionally substituted amino, COOH, lower alkyl, lower alkenyl, lower alkynyl, aryl, lower alkoxy, aryloxy, aralkyl, aralkoxy or a reporter group (RG);
R3,R4 = H, OH, optionally substituted thio, optionally substituted amino, lower alkoxy, lower alkenyloxy, lower alkynyloxy, protective group or RG;
R5 = H, OH, optionally substituted thio, optionally substituted amino, reactive 3- or 5-valent phosphorus group (e.g. phosphoramidite or H-phosphonate function), cleavable ester or amide residue or RG, or
R4 + R5 = a bond between C-2' and C-3' or an acetal function;

R6 = H, OH, optionally substituted thio or optionally substituted amino;

R7 = H, mono-, di- or triphosphate group (or alpha -, beta - or gamma -thiophosphate analogues of these phosphate esters) or a protecting group;

X = methylene or methine group substituted by halo, OH, optionally substituted thio, optionally substituted amino, COOH, lower alkyl, lower alkenyl, lower alkynyl, aryl, lower alkoxy, aryloxy, aralkyl, aralkoxy, O or RG;

n = 0 or 1;

Z = N or C provided that:

(i) if Z = N then m = 0 (N.B. no general definition of m is given); (ii) if X = optionally (sic) substituted methylene or substituted methine, then Z is not C , and

(iii) if X = O then Z is not N.

Also new are oligonucleotides and nucleic acids which incorporate at least 1 (I).

USE - (I) are substrates for DNA- and RNA-polymerases which are used for labelling or detecting nucleic acids, in DNA sequencing or in in situ hybridisation or for chemical synthesis of oligonucleotides (all claimed).

ADVANTAGE - When compared with natural nucleosides and nucleotides, (I) have higher chemical stability (towards e.g. acidic pH conditions) and higher stability to endo- or exonuclease enzymes (e.g. those contained in biological samples for nucleic acid analysis).

(I) are efficiently incorporated in nucleic acids by suitable polymerases (e.g. in nick translation or random primed labelling processes), allowing labelling by a wide range of signal groups for detection at acceptable wavelengths. (I) are also readily incorporated in long-chain oligonucleotides or nucleic acids by automated solid phase synthesis.

Dwg.0/1

11/AB/16 (Item 7 from file: 351)
DIALOG(R)File 351:Derwent WPI

011713813
WPI Acc No: 1998-130723/199812
XRAM Acc No: C98-043277
Detection of target DNA sequences - using a labelled ribo-oligonucleotide and kinetic analysis of released fragments obtained using ribo-nucleic acid nuclease
Patent Assignee: WINGER E E (WING-I)
Inventor: HARGROVE D E; KESSLER D J; WINGER E E
Number of Countries: 078 Number of Patents: 004
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 9804738	A1	19980205	WO 97US12211	A	19970724	199812	B
AU 9737994	A	19980220	AU 9737994	A	19970724	199828	
US 5853990	A	19981229	US 96687662	A	19960726	199908	
CN 1236395	A	19991124	CN 97197568	A	19970724	200014	

Priority Applications (No Type Date): US 96687662 A 19960726
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 9804738	A1	E	27	C12Q-001/68	

Designated States (National): AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH HU IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA

UG UZ VN YU ZW
Designated States (Regional): AT BE CH DE DK EA ES FI FR GB GH GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW

AU 9737994	A	C12Q-001/68	Based on patent WO 9804738
CN 1236395	A	C12Q-001/68	
US 5853990	A	C12Q-001/68	

Abstract (Basic): WO 9804738 A

Detection of a target DNA sequence in a sample comprises: (a) contacting and annealing a probe comprising a ribo- oligonucleotide (RON) attached to a first label with a sample containing a target single-stranded DNA sequence having a region complementary to the probe; (b) cleaving at least 1 of the ribonucleotides of the annealed probe with a ribo- nucleic acid nuclease capable of hydrolysing ribonucleotides in a double stranded RNA : DNA duplex to release labelled RON fragments, and (c) making sequential measurements of the release of labelled fragments to permit the kinetic characterisation of target DNA sequence; where steps (a)-(c) are performed in a single reaction mixture.

The probe is a chimeric nucleotide, preferably RNA : DNA : RNA oligonucleotide . The method further comprises the ribo- oligonucleotide attached to a second label where the first and second labels comprise interactive signal -generating moieties such that attachment of the labels causes the second label to suppress detection of the first label. The first label comprises a reporter fluorescent dye and the second label comprises a quencher fluorescent dye and the step of measuring the release of labelled ribo- oligonucleotide fragments comprises detecting reporter fluorescence.The reporter and the quencher are separated by < 10 nucleotides. The probe has a secondary structure that brings the reporter and quencher into close proximity prior to the step of annealing the probe to the target DNA sequence. Preferably, the method is for detecting a target DNA sequence comprising a first strand complementary to a second strand and which is undergoing amplification.

USE - The method can be used for the detection of specific DNA sequences, e.g. for diagnosis of disease.

ADVANTAGE - Using the kinetic analysis, the quantitative assessment of the development of signal can greatly increase the accuracy of amplification systems by revealing problems such as false positives or other false quantifications.

Dwg.0/1

11/AB/17 (Item 8 from file: 351)
DIALOG(R)File 351:Derwent WPI

009998257
WPI Acc No: 1994-265968/199433
Related WPI Acc No: 1990-058372; 1998-110620
XRAM Acc No: C94-121644
Detecting spatial relation between mRNA and gene in nucleus - by in-situ hybridisation with mRNA-specific probe without denaturing DNA
Patent Assignee: UNIV MASSACHUSETTS MEDICAL CENT (UYMA-N); UNIV MASSACHUSETTS (UYMA-N)
Inventor: JOHNSON C V; LAWRENCE J B; XING Y; SINGER R H
Number of Countries: 005 Number of Patents: 004
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
EP 612851	A1	19940831	EP 94610009	A	19940214	199433	B
US 5563033	A	19961008	US 85790107	A	19851022	199646	

			US 88257066	A	19881018		
			US 92832667	A	19920206		
			US 9323953	A	19930226		
US 5985549	A	19991116	US 85790107	A	19851022	200001	N
			US 88257066	A	19881013		
			US 92832667	A	19920206		
			US 93150767	A	19931112		
			US 94316809	A	19941003		
US 6242184	B1	20010605	US 88257066	A	19881013	200133	N
			US 92832667	A	19920206		
			US 93150767	A	19931112		
			US 94316809	A	19941003		
			US 99259099	A	19990225		

Priority Applications (No Type Date): US 9323953 A 19930226; US 85790107 A 19851022; US 88257066 A 19881018; US 92832667 A 19920206; US 94316809 A 19941003; US 99259099 A 19990225

Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
EP 612851	A1	E	16	C12Q-001/68	
Designated States (Regional): DE DK FR GB					
US 5563033	A		12	C12Q-001/68	CIP of application US 85790107
					Cont of application US 88257066
					CIP of application US 92832667
US 5985549	A			C12Q-001/68	CIP of application US 85790107
					Cont of application US 88257066
					Cont of application US 92832667
					Cont of application US 93150767
US 6242184	B1			C12Q-001/68	Cont of application US 88257066
					Cont of application US 92832667
					Cont of application US 93150767
					Cont of application US 94316809
					Cont of patent US 5985549

Abstract (Basic): EP 612851 A

An in-situ hybridisation method for detecting a specific mRNA in spatial correlation with a corresp. gene comprises: (a) hybridising nuclear RNA to a labelled on mRNA-specific nucleotide probe under conditions in which DNA is not denatured; (b) generating a signal from the label ; and (c) detecting the signal as a focus or track of fluorescence as an indication of the spatial correlation of the mRNA to the gene. Also claimed is a method as above comprising: (a) hybridising nuclear RNA to an mRNA-specific nucleotide probe tagged with a first label, under conditions in which DNA is not denatured; (b) generating a first signal from the first label; (c) fixing the cell so that the first signal is maintained at the site of transcription of the mRNA in the form of a focus or track of fluorescence; (d) hybridising the gene to a DNA -specific nucleotide (probe) tagged with a second label, under DNA -denaturing conditions; (e) generating a second signal from the second label; and (f) detecting the first and second signals as an indication of the spatial correlation of the mRNA to the gene.

USE/ADVANTAGE - The methods may be used to visualise the intranuclear distribution of mRNA produced by expression of a specific gene (mRNA transcripts in mammalian cells are localised at the site of transcription and not free to diffuse in the nucleus), to compare the levels of expression of specific alleles of a gene, to determine whether viral infections are latent or productive (latent if mRNA track is present only in the nucleus), and to detect and quantify expression of exogenous genes. The methods increase the sensitivity and stability of in-situ hybridisation to a point where labile mRNA mols. of very low

abundance, previously undetectable in the cytoplasm, can be detected in the nucleus.

Dwg.0/4

Abstract (Equivalent): US 5563033 A

An in situ hybridization method for simultaneously detecting in a cell nucleus a DNA sequence associated with a selected gene and mRNA transcribed from within the selected gene, comprising the steps of:

(a) permeabilising the cell nucleus while minimizing mRNA degradation;

(b) fixing the cells a first time, with a fixative such that the nucleus remains penetrable by labelled probes, and the nucleic acids are preserved in place;

(c) hybridizing the fixed cells a first time, under conditions that do not denature DNA, with an RNA-specific probe able to hybridize to an mRNA transcript from the selected gene without substantial hybridization to other RNA molecules present in the cell, said RNA-specific probe bearing a first label;

(d) fixing the cells a second time, to preserve during a second hybridisation RNA-probe hybrids formed during the first hybridization;

(e) denaturing the nuclear DNA in the cells;

(f) hybridizing the fixed cells a second time with a DNA-specific probe able to hybridize to a DNA sequence associated with the selected gene, without substantial hybridization to non-selected sequences, said DNA-specific probe bearing a second label distinguishable from the first label; and

(g) simultaneously detecting said first label on said RNA-specific probe as a focus or track, and said second label on said DNA-specific probe as a point, said focus or track and said point being within about 2 mum of each other;

wherein said DNA sequence associated with the selected gene comprises chromosomal nucleotide sequences on the same chromosome and within approximately 2 mum of the selected gene from which said mRNA is transcribed.

(Dwg.0/4)

11/AB/18 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0276773 DBA Accession No.: 2002-00275 PATENT

Novel homogenous method for detecting polynucleotides by using an oligonucleotide probe labeled with an environmental sensitive label , the signal of which varies upon hybridization of probe with target polynucleotide - DNA probe for polymerase chain reaction and hybridization

AUTHOR: Nurmi J

CORPORATE SOURCE: Turku, Finland.

PATENT ASSIGNEE: Nurmi J 2001

PATENT NUMBER: WO 200161034 PATENT DATE: 20010823 WPI ACCESSION NO.: 2001-522603 (200157)

PRIORITY APPLIC. NO.: FI 2000333 APPLIC. DATE: 20000216

NATIONAL APPLIC. NO.: WO 2001FI128 APPLIC. DATE: 20010213

LANGUAGE: English

ABSTRACT: Homogenous detection of a target polynucleotide (tPN) in a sample is new, by contacting a sample of PN with labeled (with a an environmental sensitive fluorescent lanthanide chelate label) DNA probe and detecting the hybridization between the DNA probe and tPN by measuring signal intensity by timed resolved fluorometry. The above can be used to detect target polynucleotide including ss or ds DNA or RNA or their derivatives, a hybrid of DNA and RNA and

nucleic acid derivatives such as peptide nucleic acid in a sample. In an example, a specified DNA probe was modified and labeled. DNA probes Tb1093 and Tb1093S were purified by HPLC and mixed with target oligonucleotide . Tb signals were recorded immediately after mixing at 545 nm. Tb signals of all mixtures were recorded. Tb1093 was also tested in the detection of a specific polymerase chain reaction product. A 163 bp segment of prostate-specific antigen cDNA was amplified in the presence of the DNA probe and Tb signals were recorded from each amplification well. Hybridization of the Tb labeled DNA probe with the target sequence showed a clear Tb signal increase. (45pp)

11/AB/19 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0273574 DBA Accession No.: 2001-13781 PATENT
Labeling RNA molecules by fragmenting RNA, fixing a ligand to the terminal phosphates released during fragmentation, and located at the 3' or 5' end of each RNA fragment and binding a labeling agent to the ligand - fluorescently-labeled RNA probe, DNA probe or DNA array for medical diagnosis
AUTHOR: Laayoun A; Do D; Miyada C G
CORPORATE SOURCE: Marcy L'Etoile, France; Santa Clara, CA, USA.
PATENT ASSIGNEE: Bio-Merieux; Affymetrix 2001
PATENT NUMBER: WO 200144506 PATENT DATE: 20010521 WPI ACCESSION NO.: 2001-408488 (2043)
PRIORITY APPLIC. NO.: IB 992072 APPLIC. DATE: 19991217
NATIONAL APPLIC. NO.: WO 99IB2072 APPLIC. DATE: 19991217
LANGUAGE: English
ABSTRACT: A method labeling (M1) a RNA molecule with signal amplification is new and involves fragmenting the RNA , fixing a ligand to the terminal phosphates which are released during the fragmentation, and which are located at the 3' end and/or the 5' end of each fragment of the RNA , and binding a labeling agent to the ligand. Also claimed is the RNA fragment (I) obtained by (M1). (I) is used as an RNA probe for detecting an RNA and/or a DNA or as a labeled target which is able to bind to a capture DNA probe or DNA array. The method preferably has applications in medical diagnosis. The method enables the generation of RNA fragments once the fragmentation has been completed. In addition, the fragmentation makes it possible to obtain fragments which are optimum size for a possible hybridization . Quality of the hybridization is improved and thus the post-hybridization detection of labeled fragments is more rapid and efficient. In an example, RNA from Escherichia coli MG1655 was used. (I) contains at its 3' end, a phosphate or triphosphate bearing a fluorescein bound to an anti-fluorescein antibody bearing a biotin, where the antibody is bound to a labeled streptavidin. (35pp)

11/AB/20 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0248658 DBA Accession No.: 2000-03148 PATENT
Amplifying and detecting target nucleic acids used in any amplification reaction using a pair of primers to generate double-stranded sequences - HIV virus nucleic acid detection using polymerase chain reaction, DNA primer and DNA probe
AUTHOR: Salituro J A; Carrino J L

CORPORATE SOURCE: Abbott Park, IL, USA.
PATENT ASSIGNEE: Abbott-Lab. 1999
PATENT NUMBER: WO 9960159 PATENT DATE: 19991125 WPI ACCESSION NO.: 2000-072444 (2006)
PRIORITY APPLIC. NO.: US 79675 APPLIC. DATE: 19980515
NATIONAL APPLIC. NO.: WO 99US10271 APPLIC. DATE: 19990511
LANGUAGE: English
ABSTRACT: Amplifying and detecting target nucleic acids is new and involves amplifying the target sequence from an amplification mixture containing 2 DNA primers, and detecting copies of the target sequence. The first primer is in a 15-250% excess to the 2nd. A DNA probe is hybridized to the amplification product from the 1st primer to form a hybrid complex, which if detected indicates the presence of the nucleic acid sequence. The method is useful for any amplification reaction using a pair of primers to generate ds sequences. In an example, HIV virus detection was carried out. Dilutions of HIV virus RNA were reverse transcribed, polymerase chain reaction amplified and detected with primers and a probe. When the unlabeled primer was present at lower concentrations than the labeled primer, higher signals were achieved at higher target concentrations, and signal plateauing of the signal was avoided. When unlabeled primer concentration was equal to or higher than labeled primer concentration, a hook effect was observed where a higher target concentration exhibited a lower signal. (22pp)

11/AB/21 (Item 4 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0220007 DBA Accession No.: 98-01604 PATENT
Detecting several nucleic acid targets by hybridization to immobilized, labeled capture probes - multiple DNA probe hybridization in a pattern on an adsorbent, e.g. for diagnostic applications or forensics
AUTHOR: Granados E N; Bouma S R; Carrino J J; Solomon N A
CORPORATE SOURCE: Abbott Park, IL, USA.
PATENT ASSIGNEE: Abbott-Lab. 1997
PATENT NUMBER: WO 9741256 PATENT DATE: 971106 WPI ACCESSION NO.: 97-549752 (9750)
PRIORITY APPLIC. NO.: US 639224 APPLIC. DATE: 960426
NATIONAL APPLIC. NO.: WO 97US7014 APPLIC. DATE: 970425
LANGUAGE: English
ABSTRACT: A new method for detecting multiple target sequences in a test sample involves: contacting a hybridization platform with the test sample, where the platform has at least 2 capture DNA probes immobilized on an adsorbent in a defined pattern, at least 2 probes have distinct sequences, and each is labeled with a member of a signal generating system; hybridizing at least 1 target sequence to the platform to generate a signal change; and detecting a change in signal, as an indication of the presence of a target sequence. The probe may be labeled with an intercalation dye, a PORSCHA dye, or a quenching group and a reporter group. Probes may be degraded after hybridization , using RNA -ase-H (EC-3.1.26.4), restriction endonuclease, endonuclease-IV, other endonuclease or exonuclease-III activity. Hybridized target sequences may be contacted with DNA amplification reagents, e.g. a DNA -polymerase (EC-2.7.7.7) with nuclease or exonuclease activity and NTPs. A means for stopping capture probe degradation may be present between the label and adsorbent. The method may be used in diagnostic and forensic applications. (28pp)

11/AB/22 (Item 5 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0211718 DBA Accession No.: 97-06839 PATENT
Detection of analyte in sample using nucleobase-containing probe - antibody, antigen, hapten, DNA and RNA detection by hybridization with an oligonucleotide DNA probe or RNA probe and label
AUTHOR: Weindel K
CORPORATE SOURCE: Mannheim, Germany.
PATENT ASSIGNEE: Boehr.Mannheim 1997
PATENT NUMBER: DE 19537952 PATENT DATE: 970417 WPI ACCESSION NO.: 97-227517 (9721)
PRIORITY APPLIC. NO.: DE 1037952 APPLIC. DATE: 951012
NATIONAL APPLIC. NO.: DE 1037952 APPLIC. DATE: 951012
LANGUAGE: German
ABSTRACT: A method for detecting an analyte in a sample is claimed, which involves contacting a sample with a nucleobase-containing probe, having two or more non-nucleoside labels, under conditions such that the analyte will bind directly or indirectly to the probe and detecting the bound product. Also claimed is a probe for detecting an analyte consisting of a contact-mediating region that is readily accessible to the analyte and spatially separated from a signal-mediating region containing the two or more labels. Preferably, the probe is part of a sterically demanding reaction complex, while the labeling groups are less sterically demanding. The bound product is detected via a sterically undemanding conjugate consisting of a group with affinity for the labels and a signalling group (e.g. a native or recombinant calcium-activatable photoprotein), especially where the conjugate has a mol.wt. of 100,000 o less and the 2 components are connected via a linker of at least 4 atoms. This method may be used for the detection of antibodies, antigens, haptens, RNA and DNA . The probe can be much smaller than those with signal-mediating hybridization zones. (16pp)

11/AB/23 (Item 6 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0206100 DBA Accession No.: 97-01221 PATENT
Labeled probes for nucleic acid detection - DNA probe with stem duplex for DNA or RNA detection by hybridization
AUTHOR: Tyagi S; Kramer F R; Lizardi P M
CORPORATE SOURCE: New York, NY, USA.
PATENT ASSIGNEE: Public-Health-Res.Inst.New-York 1996
PATENT NUMBER: EP 745690 PATENT DATE: 961204 WPI ACCESSION NO.: 97-013705 (9702)
PRIORITY APPLIC. NO.: US 439819 APPLIC. DATE: 950512
NATIONAL APPLIC. NO.: EP 96303544 APPLIC. DATE: 960510
LANGUAGE: English
ABSTRACT: A labeled unimolecular DNA probe for detecting at least 1 nucleic acid (NA) strand containing a preselected NA target sequence under preselected assay conditions including a detection temp. is claimed. The probe comprises: an ss target complement sequence with 6-9 (7-9) nucleotides and having a 5' terminus and 3' terminus; a stem duplex comprising a 5' arm sequence adjacent to and covalently linked to the 5' terminus and a 3' arm sequence adjacent to and covalently linked to the 3' terminus, where the arms are 3-25 nucleotides long and the duplex has a melting temp. above the detection temp. under the

preselected assay conditions; and at least 1 label pair comprising a 1st label conjugated to the probe in the vicinity of the 5' arm sequence and a 2nd label moiety proximate to the 1st label moiety and conjugated to the probe in the vicinity of the 3' arm sequence. The probe has a characteristic signal whose level is a function of the degree of interaction of the 1st and 2nd labels , where the signal has 2 levels at 10 deg below, 10 deg above the melting temp. and a 3rd level at the detection temp. Also claimed are a kit and assay for detecting NA. (41pp)

11/AB/24 (Item 7 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0191943 DBA Accession No.: 96-03346 PATENT
Sensitive detection of target nucleic acid with linear signal amplification - DNA probe hybridization and cleavage in binding region, followed by hybridization with a matrix nucleic acid; diagnostic application
AUTHOR: Seibl R; Rosemeyer V
CORPORATE SOURCE: Mannheim, Germany.
PATENT ASSIGNEE: Boehr.Mannheim 1996
PATENT NUMBER: DE 4431269 PATENT DATE: 960118 WPI ACCESSION NO.: 96-069707 (9608)
PRIORITY APPLIC. NO.: DE 4425264 APPLIC. DATE: 940716
NATIONAL APPLIC. NO.: DE 4431269 APPLIC. DATE: 940902
LANGUAGE: German
ABSTRACT: A target nucleic acid may be detected sensitively by hybridization with a DNA probe, which has target hybridizing (B1) and non- hybridizing (B2) portions. The probe may be cleaved in B1 to produce a product (B') which includes B2, followed by hybridization of B' with a matrix nucleic acid (C), which has a region (C2) which hybridizes with B' in B2 and another region (C1) which does not hybridize with B1. Hybridization between B' and C is then detected . A kit for the process contains B, C, a matrix-dependent polymerase and buffers. The target is RNA or preferably DNA from a virus, bacterium or cell, and is in solution, suspension, fixed or in cells. The method provides linear sequence-specific signal amplification with high sensitivity. The probe does not carry a label , so background signals are minimized. Since the target itself is not amplified, the risk of false positives is minimized. Thermal cycling and very stringent hybridization conditions are not needed, so the process is suitable for automation and routine use. (22pp)

11/AB/25 (Item 8 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0155694 DBA Accession No.: 93-13746 PATENT
A method for detection a compound which binds to target RNA or DNA - using an immobilized DNA probe or RNA probe
PATENT ASSIGNEE: Lilly 1993
PATENT NUMBER: EP 562765 PATENT DATE: 930929 WPI ACCESSION NO.: 93-305141 (9339)
PRIORITY APPLIC. NO.: US 857205 APPLIC. DATE: 920325
NATIONAL APPLIC. NO.: EP 93302065 APPLIC. DATE: 930318
LANGUAGE: English
ABSTRACT: A method for detecting compounds that bind to a target polynucleotide comprises: (1) fixing a target polynucleotide to a solid surface, which comprises or is contained within a container system; (2)

forming an entity of the target polynucleotide bound by a compound which blocks hybridization of a second polynucleotide (which is complementary to the target polynucleotide and has a detectable label attached); (3) causing the label to give off a signal ; and (4) detecting reduction in the signal relative to a control. Preferably, a target polynucleotide bound to a ligand recognized by the receptor is complexed to the receptor between steps (1) and (2); a complex is formed between the 2nd ligand and 2nd receptor (which is labeled) between steps (2) and (3); and/or a complex is formed between the ligand and the receptor (which is labeled) between steps (2) and (3). The target polynucleotide is preferably DNA or RNA . The signal is detected by spectrophotometry, radioactive, electrical, fluorescent or magnetic techniques. The method may be used to detect organisms and their residues e.g. HIV virus-1 rev protein in the supernatant of cultured cells. (10pp)

11/AB/26 (Item 9 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0133558 DBA Accession No.: 92-06050 PATENT
Detection of specific target molecules - e.g. DNA , RNA , protein, peptide, lipoprotein, carbohydrate, fat detection involves DNA probe hybridization to phagemid, expression in transformant and detection of streptavidin, biotin label
PATENT ASSIGNEE: City-Of-Hope 1992
PATENT NUMBER: US 5085982 PATENT DATE: 920204 WPI ACCESSION NO.: 92-064402 (9208)
PRIORITY APPLIC. NO.: US 873504 APPLIC. DATE: 860612
NATIONAL APPLIC. NO.: US 873504 APPLIC. DATE: 860612
LANGUAGE: English
ABSTRACT: The presence of a target molecule (I) is detected by: i. binding (I) to a substrate; ii. combining (I) with a probe, the probe bearing 1 of a pair of moieties which bind inter se; iii. binding the (I)-probe combination to a phagemid bearing the other 1 of the pair of moieties which bind inter se, the plasmid portion of the phagemid containing a signal encoding DNA, e.g. a luciferase or beta-galactosidase (EC-3.2.1.23) signal sequence; iv. transfecting the phagemid into a lysogenic cell to express the signal encoding DNA present in the plasmid portion of the phagemid; v. replicating the transfected cell; vi. detecting expression of the signal encoding DNA; and vii. relating the detected signal to the presence of (I). The pair of moieties that bind inter se may consist of e.g. streptavidin and biotin. The method can be used for the detection and quantification of DNA, RNA, proteins, peptides, lipoproteins, carbohydrates, fats, etc. The method uses a signal amplification system comprising living cells which are specifically provided with the ability to survive and reproduce and then are detected in the event that (I) is present. (9pp)

11/AB/27 (Item 10 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0119047 DBA Accession No.: 91-06689 PATENT
Detection of polynucleotide sequence - DNA or RNA hybridization method by fixing target on solid adsorbent and hybridizing with a DNA probe or RNA probe with a label which can generate a soluble signal
PATENT ASSIGNEE: Enzo-Biochem. 1991
PATENT NUMBER: US 4994373 PATENT DATE: 910219 WPI ACCESSION NO.:

91-072902 (9110)
PRIORITY APPLIC. NO.: US 732374 APPLIC. DATE: 850509
NATIONAL APPLIC. NO.: US 385986 APPLIC. DATE: 890720
LANGUAGE: English
ABSTRACT: A new method for detection of target DNA or RNA comprises: fixing the DNA or RNA to a solid adsorbent, comprising or contained within a transparent or translucent non-porous system, so that single-stranded DNA or RNA is capable of hybridizing to a complementary sequence; forming a hybrid with a DNA or RNA probe which has an attached chemical label which generates a soluble signal ; and generating and detecting the soluble signal. The solid adsorbent may be e.g. glass, polystyrene, polyethylene, dextran or polypropylene. The signalling moiety may be attached to the probe by formation of a complex of e.g. biotin and avidin, biotin and streptavidin or a sugar and a lectin. Part of the solid adsorbent may be modified to facilitate fixing of the DNA or RNA , by: heating or boiling in dilute nitric acid for 45 min; washing with distilled water; drying at 115 deg for 24 hr; incubating in contact with 10% gamma-aminopropyltriethoxysilane for 2-3 hr at 45 deg; washing with water; and drying overnight at 100 deg. Generation of a soluble signal allows simple and rapid visual detection of the target sequence, and also allows quantification. (9pp)

11/AB/28 (Item 11 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res

0118454 DBA Accession No.: 91-06096 PATENT
Amplification of target sequence by preparation of product with polynucleotide tail - primer extension or polymerase chain reaction product tailing for e.g. solid-phase capture or label attachment
PATENT ASSIGNEE: ICI 1991
PATENT NUMBER: EP 416817 PATENT DATE: 910313 WPI ACCESSION NO.: 91-075303 (9111)
PRIORITY APPLIC. NO.: GB 8920097 APPLIC. DATE: 890906
NATIONAL APPLIC. NO.: EP 90309502 APPLIC. DATE: 900830
LANGUAGE: English
ABSTRACT: A new method for amplification of a target RNA or DNA sequence by the polymerase chain reaction comprises contacting the sequence under hybridization conditions, together or sequentially, with a first DNA primer (A) and a corresponding amplification DNA primer (B), nucleotides and a DNA -polymerase (EC-2.7.7.7). (A) and/or (B) comprise a region complementary to the target, and a polynucleotide tail. (A) and/or (B) may be subjected to primer extension using the target as template. After denaturation of the extension product, primer extension may be carried out further to form an amplified product. The target binding region and the polynucleotide tail may be separated by a blocking moiety, e.g. ribofuranosyl naphthalene, deoxyribofuranosyl naphthalene, metaphosphate or straight chain C6-20 alkylene moieties, or at least 2 nucleotide methylphosphonate or nucleotide phosphoramidate moieties. The tailed products may be used for solid-phase capture or for linkage to a label or signal system. The method is applicable to disease diagnosis and research, for detection of microorganisms or mutations. (36pp)
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=> d stat que
L1        27471 SEA FILE=REGISTRY RIBONUCLEIC ACID?/CN
L3       322173 SEA FILE=HCAPLUS RIBONUCLEIC(W)ACID? OR RNA OR L1
L7        27563 SEA FILE=HCAPLUS L3(L)(?HYBRID? OR CAPTUR?(3W)REAGENT? OR
                DENDRIMER?)
L9           49 SEA FILE=HCAPLUS L7 (L)LABEL?(5A)SIGNAL?
L10           6 SEA FILE=HCAPLUS L9(L)GENE?(W)EXPRESS?


=> d ibib abs hitrn l10 1-6

L10  ANSWER 1 OF 6  HCAPLUS  COPYRIGHT 2002 ACS
ACCESSION NUMBER:         2002:141437  HCAPLUS
TITLE:                    In situ hybridization: Detection of DNA and RNA
AUTHOR(S):                Jin, Long; Qian, Xiang; Lloyd, Ricardo V.
CORPORATE SOURCE:         Mayo Clinic and Foundation, Rochester, MN, USA
SOURCE:                   Morphology Methods (2001), 27-46.  Editor(s): Lloyd,
                          Ricardo V.  Humana Press Inc.: Totowa, N. J.
                          CODEN: 69CHF5; ISBN: 0-89603-955-2
DOCUMENT TYPE:            Conference; General Review
LANGUAGE:                 English
AB   A review discusses the basic principles and approaches of the in situ
     hybridization (ISH) technique, new advances in the ISH method, and
     some application of ISH methods for the study of specific diseases.  The
     main advantages of the ISH method are its specificity for individual cells
     in a heterogeneous tissue or cell population, and its sensitivity in
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detecting low-copy **gene expression** in cells or chromosomal gene mapping. ISH comprises multiple steps including probe prepn. and **labeling**, tissue prepn., **hybridization**, and **signal** detection. Three principal types of probes can be used for ISH, including double-stranded complementary DNA probes, single-stranded antisense **RNA** probes, and synthetic oligonucleotide probes.

REFERENCE COUNT: 90 THERE ARE 90 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 2 OF 6 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:72313 HCAPLUS
DOCUMENT NUMBER: 136:97287
TITLE: Labeling of mRNA with dendrimers for use as probes for microarrays in gene expression profiling and high-throughput functional genomics
INVENTOR(S): Getts, Robert C.; Kadushin, James M.
PATENT ASSIGNEE(S): Genisphere Inc, USA
SOURCE: PCT Int. Appl., 41 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002006511	A2	20020124	WO 2001-US22818	20010719
WO 2002006511	A3	20020411		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2000-219397P P 20000719

AB The present invention is directed to a method for detg. the presence of a specific nucleotide sequence in a mRNA of a target sample. An advantage of the present invention is that it does not require the time and labor consuming conversion of sample **RNA** into cDNA. The first component comprises a mRNA reagent, extd. directly from a target sample, contg. a target nucleotide sequence and a capture sequence. The second component is a **capture reagent** having at least one first arm contg. a **label**, capable of emitting a detectable **signal**, and at least one second arm having a nucleotide sequence complementary to a capture sequence attached to the **RNA** reagent on a microarray. A pre-**hybridized RNA-capture reagent** complex is generated by **hybridization** of the capture sequence of the mRNA with the complementary sequence on the second arm of the **capture reagent**, wherein the incubation of the two components is performed between 45-60.degree. for 15 min to 24 h. The pre-**hybridized RNA-capture**

reagent complex is then contacted with a microarray, having a plurality of probe sequences. **Hybridization** of the target nucleotide sequences of the pre-**hybridized RNA-capture reagent** complex to the probe occurs following incubation at 45-65.degree. for 15 min to 24 h. **Unhybridized RNA/capture reagent** complexes are removed from microarray by washing. A detectable signal is emitted from the **hybridized** complex. The microarray surface can be regenerated by washing with a 0.05 M sodium hydroxide soln. at a temp. between 50-60.degree., which separates the **hybridized** mRNA from the probes. Alternatively, the target **RNA** contg. the capture and target nucleotide sequences can be first **hybridized** to oligonucleotide probes on the microarray and then this complex can be **hybridized** to the **capture reagent**.
Capture reagents include **dendrimers**, carbohydrates, proteins and nucleic acids. This method is useful for improving sensitivity, generating low background noise and minimizing false pos. results using microarrays. This invention has uses in **gene expression** profiling and high-throughput functional genomics.

L10 ANSWER 3 OF 6 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1998:309365 HCAPLUS
DOCUMENT NUMBER: 129:134428
TITLE: Study of expression of gene encoding Ki-67 antigen in human pancreatic cancer using non-radioactive in situ hybridization and immunohistochemistry
AUTHOR(S): Wu, Yulian; Peng, Shuyou; Sheng, Hongwei
CORPORATE SOURCE: Surgical Laboratory, Second Affiliated Hospital, Zhejiang Medical University, Hangzhou, 310009, Peop. Rep. China
SOURCE: Chin. Med. J. (Beijing, Engl. Ed.) (1997), 110(11), 869-874
CODEN: CMJODS; ISSN: 0366-6999
PUBLISHER: Chinese Medical Association
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Whether the **gene expression** of the Ki-67 protein in pancreatic carcinoma specimens is altered was studied at transcriptional and translational level in situ. Forty pancreatic cancer, 5 normal pancreatic and 4 chronic pancreatitis tissues were used in this study. A 435 bp cDNA fragment located in codon 2, exon 13 of Ki-67 antigen gene was amplified by PCR. The DIG (digoxigenin)-labeled cRNA probes were transcribed with 2 com. DIG **RNA** labeling kit. Localization of the Ki-67 protein and the specific mRNA was performed by combining IHC (immunohistochem.) with DIG-labeled in situ **hybridization**. Localization of the Ki-67 protein and mRNA in pancreatic tissue sections was first successfully accomplished. Anal. of the Ki-67 mRNA transcription in 17 pancreatic cancer specimens with Ki-67 IHC **labeling** index >20% revealed stronger mRNA **signals** in poorly differentiated specimens with Ki-67 index >50% than in well-differentiated cases with the IHC labeling index of 20-50%. A high expression of both the mRNA and the protein was obsd. in pancreatic adenocarcinoma with poor differentiation. The abnormal overexpression of

the Ki-67 protein might be correlated with the central part, exon 13, of the gene.

L10 ANSWER 4 OF 6 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1997:185614 HCAPLUS
DOCUMENT NUMBER: 126:288614
TITLE: Signal amplification in the detection of single-copy DNA and RNA by enzyme-catalyzed deposition (CARD) of the novel fluorescent reporter substrate Cy3.29-tyramide
AUTHOR(S): Schmidt, Brigitte F.; Chao, Jean; Zhu, Zhengrong; DeBiasio, Robin L.; Fisher, Gregory
CORPORATE SOURCE: Center Light Microscope, Imaging & Biotechnology, Carnegie Mellon Univ., Pittsburgh, PA, USA
SOURCE: Journal of Histochemistry and Cytochemistry (1997), 45(3), 365-373
CODEN: JHCYAS; ISSN: 0022-1554
PUBLISHER: Histochemical Society, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The catalyzed reporter deposition (CARD) method, utilizing the novel fluorescent reporter Cy3.29-tyramide, is successful in fluorescent in situ **hybridization** (FISH) detection of **RNA** and single-copy DNA. Histone 4 expression is detected in **RNA** exts. of S-phase, synchronized HeLa cells by dot-blot anal. **Gene expression** of histone 4 in HeLa cells is demonstrated by FISH via CARD, utilizing oligonucleotide probes. Fluorescence intensity measurements on CARD-amplified histone 4 **RNA** detection showed (a) a 25-fold amplification of the signal brightness by biotinylated oligonucleotide probes and (b) a sixfold amplification of the **signal** brightness by horseradish peroxidase (HRP)-**labeled** histone 4 probes vs. the directly stained control. The sensitivity of the CARD method is demonstrated by the FISH detection of single-copy DNA on human corneal fibroblast and HeLa S3 interphase nuclei. Chromosomal localization of the single copy DNA is demonstrated on HeLa S3 metaphase chromosome spreads.

L10 ANSWER 5 OF 6 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1995:1003703 HCAPLUS
DOCUMENT NUMBER: 124:106305
TITLE: Increased expression of synapsin I mRNA in defined areas of the rat central nervous system following chronic morphine treatment
AUTHOR(S): Matus-Leibovitch, Noa; Ezra-Macabee, Vittoria; Saya, Daniella; Attali, Bernard; Avidor-Reiss, Tomer; Barg, Jacob; Vogel, Zvi
CORPORATE SOURCE: Department of Neurobiology, The Weizmann Institute of Science, Rehovot, 76100, Israel
SOURCE: Mol. Brain Res. (1995), 34(2), 221-30
CODEN: MBREE4; ISSN: 0169-328X
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Chronic opiate administration leads to a selective regulation of several cellular proteins and mRNAs. This phenomenon has been viewed as a

compensatory mechanism to the opiate signaling leading to the development of opiate addiction. In this study, in situ **hybridization** histochem. expts. were employed to investigate the effect of chronic morphine treatment on synapsin I **gene expression**. The authors show here for the first time that prolonged morphine exposure causes a selective increase in the mRNA levels of synapsin I in several brain regions which are considered to be important for opiate action. Quant. anal. of the **signals**, obtained by **hybridization** of digoxigenin-**labeled** antisense **RNA** probe, revealed a 5.8- and 7-fold increase of synapsin I mRNA levels in the locus coeruleus and the amygdala of morphine-treated rats, resp., as compared with control untreated rats. Increased expression of synapsin I mRNA was also obsd. in the spinal cord of morphine-treated rats (by 3.8-fold). Since opiates were shown to attenuate neurotransmitter release and reduce synapsin I phosphorylation, it is suggested that the increase in synapsin I levels would lead to the requirement of higher amts. of opiate agonists to obtain the opiate physiol. effects. These results suggest that the increases in mRNA levels of synapsin I in these specific areas can be part of the mol. mechanism(s) underlying opiate tolerance and withdrawal.

L10 ANSWER 6 OF 6 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1995:523874 HCAPLUS
DOCUMENT NUMBER: 122:256498
TITLE: Detection of in situ localization of long form prolactin receptor messenger RNA in lactating rats by biotin-labeled riboprobe
AUTHOR(S): Shirota, Mariko; Kurohmaru, Masamichi; Hayashi, Yoshihiro; Shirota, Kinji; Kelly, Paul A.
CORPORATE SOURCE: Hatano Research Institute, Food and Drug Safety Center, Kanagawa, 257, Japan
SOURCE: Endocr. J. (Tokyo) (1995), 42(1), 69-76
CODEN: ENJOEO; ISSN: 0918-8959
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Biotinylated riboprobe that specifically **hybridized** with mRNAs encoding the long form of prolactin receptor (PRLRL) was transcribed from 269 bp Hind III and Xho I fragment of the cytoplasmic domain of PRLRL complementary DNA (cDNA). The probe was used for in situ **hybridization** to identify tissue localization of PRLRL mRNA in the mammary gland, liver, ovaries and kidneys from lactating rats at 24-36 h after delivery. Histochem. detection of **signals** by horseradish peroxidase (HRP)-**labeled** streptavidin revealed that the PRLRL gene was expressed on the alveolar epithelial cells and mammary ductal epithelium in the mammary gland, and hepatocytes in the liver. In the ovary, the PRLRL gene was expressed on the luteal cells in the newly formed corpus luteum, granulosa cells and theca cells of follicles at various stages of development, hypertrophied theca cells in the atretic follicle, and secondary interstitial cells, but no signal was obsd. in the kidney. Biotinylated sense **RNA** probe did not detect any signals in any of the tissues examd. In situ **hybridization** with non-radiolabeled probe provided the identification of PRLRL mRNA in the fine tissues, such as follicular epithelium in the ovary, and showed the morphol. of individual cells expressing the PRLRL gene. In particular, the diversity of signal intensity in the same mammary gland with different

appearances suggested the existence of a local mechanism controlling PRLRL **gene expression**.

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=> d stat que
L1        27471 SEA FILE=REGISTRY RIBONUCLEIC ACID?/CN
L2           34 SEA FILE=REGISTRY NUCLEIC ACID?/CN
L3       322173 SEA FILE=HCAPLUS RIBONUCLEIC(W)ACID? OR RNA OR L1
L4      1315800 SEA FILE=HCAPLUS NUCLEIC(W)ACID? OR NA OR DNA OR L2
L7        27563 SEA FILE=HCAPLUS L3(L)(?HYBRID? OR CAPTUR?(3W)REAGENT? OR
                DENDRIMER?)
L8           67 SEA FILE=HCAPLUS L7 AND LABEL?(5A)SIGNAL?
L9           49 SEA FILE=HCAPLUS L7 (L)LABEL?(5A)SIGNAL?
L10           6 SEA FILE=HCAPLUS L9(L)GENE?(W)EXPRESS?
L11          49 SEA FILE=HCAPLUS L8 AND L4
L12          45 SEA FILE=HCAPLUS L11 NOT L10
L13          30 SEA FILE=HCAPLUS L9 AND L12
L14           4 SEA FILE=HCAPLUS L13 AND GENE?(5A)EXPRESS?
L15           4 SEA FILE=HCAPLUS L14 NOT L10


=> d ibib abs hitrn l15 1-4

L15 ANSWER 1 OF 4  HCAPLUS  COPYRIGHT 2002 ACS
ACCESSION NUMBER:         2002:221153  HCAPLUS
DOCUMENT NUMBER:          136:258285
TITLE:                    Detection of nucleic acids by
                          hybridization to immobilized probes followed by
                          labeling of the hybrid for signal
                          amplification
INVENTOR(S):              Yang, Li; Wang, Xun; Zhu, Tong; Shi, Liang
PATENT ASSIGNEE(S):       USA
SOURCE:                   U.S. Pat. Appl. Publ., 18 pp., Cont.-in-part of U. S.
                          Ser. No. 565,214, abandoned.
                          CODEN: USXXCO
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   2
PATENT INFORMATION:

     PATENT NO.        KIND  DATE          APPLICATION NO.  DATE
     ---------------   ----  --------      ---------------  --------
     US 2002034753      A1   20020321      US 2001-863527   20010514
PRIORITY APPLN. INFO.:                   US 2000-565214   B2 20000504
AB   Currently, three technologies are utilized for anal. of gene
     expression: hybridization-based technologies, PCR-based
     technologies, and sequence-based technologies.  The present invention
     provides a method for analyzing the presence and/or amt. of a specific
     nucleic acid using a solid support and a capture probe
     complementary to a region of a target nucleic acid,
     and polymg. a labeled extension complementary to the target
     nucleic acid.  The invention provides a method of anal.
     of all types of nucleic acids, and can be used to
     study multiple genes in a single assay using different capture probes
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conjugated to different class of microspheres that can be mixed in any desired combination. The method involves capturing the **nucleic acid** with immobilized probes. The hybrid can then be labeled by a hybrid-dependent process, such as primer extension, PCR, biotin-avidin interaction, or immunoassay that leads to signal amplification. Alternatively, a second probe carrying a reporter group can be hybridized to the partially single stranded complex. This second hybridization may be detected by another signal amplification method.

IT **9014-24-8**, **RNA** polymerase
RL: ARU (Analytical role, unclassified); CAT (Catalyst use); ANST (Analytical study); USES (Uses)
(for probe modification in **hybrids**; detection of **nucleic acids** by **hybridization** to immobilized probes followed by **labeling** of **hybrid** for **signal** amplification)

L15 ANSWER 2 OF 4 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:286401 HCAPLUS
DOCUMENT NUMBER: 136:32307
TITLE: Preparation of nonradioactive probes for in situ hybridization
AUTHOR(S): Abraham, Timothy W.
CORPORATE SOURCE: Ambion, Inc., Austin, TX, 78744, USA
SOURCE: Methods (San Diego, CA, United States) (2001), 23(4), 297-302
CODEN: MTHDE9; ISSN: 1046-2023
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In situ **hybridization** (ISH) enables the precise localization of **RNA** targets and provides an avenue to study the temporal and spatial patterns of **expression** of specific **genes**. ISH has evolved from being an esoteric technique to one that is routinely used by researchers in many areas of research. A major driving force has been the development of numerous nonisotopic **labeling** and **signal** detection methods. Historically, radioactive probes and autoradiog. provided sensitivity that was unattainable with nonisotopic probes. But the long exposure times required for signal detection and the perceived dangers assocd. with radioactivity limit its use. Advances in nonisotopic detection systems have overcome many of the limitations assocd. with using radiolabeled probes. One of the most significant contributions from nonisotopic methods is the ability to discriminate between multiple **nucleic acid** sequences simultaneously. (c) 2001 Academic Press.

REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 3 OF 4 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1987:192077 HCAPLUS
DOCUMENT NUMBER: 106:192077
TITLE: Modulation of tyrosine hydroxylase **gene expression** in the central nervous system visualized by in situ hybridization
AUTHOR(S): Berod, Anne; Faucon Biguet, Nicole; Dumas, Sylvie;

Bloch, Bertrand; Mallet, Jacques
CORPORATE SOURCE: Hop. Sainte-Eugenie, Saint-Genis-Laval, F-69230, Fr.
SOURCE: Proc. Natl. Acad. Sci. U. S. A. (1987), 84(6), 1699-703
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A rat tyrosine hydroxylase (EC 1.14.16.2) cDNA probe was used for in situ **hybridization** studies on histol. sections through the locus coeruleus, substantia nigra, and the ventral tegmental area of the rat brain. Exptl. conditions were established that yielded no background and no signal when pBR322 was used as a control probe. Using the tyrosine hydroxylase probe, the specificity of the labeling over catecholaminergic cells was ascertained by denervation expts. and comparison of the **hybridization** pattern with that of immunoreactivity. The use of 35S-**labeled** probe enabled the **hybridization signal** to be resolved at the cellular level. A single injection of reserpine into the rat led to an increase of the intensity of the autoradiog. signal over the locus coeruleus area, confirming an **RNA** gel blot anal. The potential of in situ **hybridization** to analyze patterns of modulation of gene activity as a result of nervous activity is discussed.

L15 ANSWER 4 OF 4 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1983:138392 HCAPLUS
DOCUMENT NUMBER: 98:138392
TITLE: Use of a cDNA library for the study of mRNA changes during muscle differentiation
AUTHOR(S): Devlin, Robert B.; Haskell, Sally G.
CORPORATE SOURCE: Dep. Biol., Emory Univ., Atlanta, GA, 30322, USA
SOURCE: Dev. Biol. (1983), 95(2), 476-83
CODEN: DEBIAO; ISSN: 0012-1606
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A cDNA library was used to measure changes in many individual mRNAs during muscle differentiation in culture. A library of 1000 clones was constructed from total myofiber poly(A) **RNA**. About 23% of these clones gave a detectable colony **hybridization signal** with end-**labeled** myofiber mRNA; the remainder contained muscle sequences too rare to be detected with this assay. The 230 pos. clones were grouped into 4 classes based on relative visual intensity. Reconstruction expts. using pure globin mRNA enabled detn. of the approx. percentage of total **RNA** made up by each mRNA **hybridizing** to a cDNA clone. Those clones contg. sequences complementary to developmentally regulated mRNAs were identified by a differential **hybridization** procedure. The cDNA library was screened with end-labeled mRNA from both undifferentiated myoblasts and differentiated myofibers. Although the bulk of the clones **hybridized** essentially the same with both **RNA** populations, several dozen were found which **hybridized** differentially. Some clones contained sequences which were not present in myoblasts and present in very high quantities in myofibers. Others contained sequences found in both myoblasts and myofibers but in increased quantities in the differentiated cells. Still others contained sequences which decreased in

quantity during muscle differentiation. The clones in the 1st group were chosen for immediate anal. since they likely contain contractile protein mRNA sequences. However, all characterized cDNA clones can be used as probes to study the chromosomal organization and developmental **expression** of **genes** active during muscle differentiation.